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C	83	21.6	0.9	54	16	AAT23964	Human gene signature
C	84	21.6	0.9	24	ABN36856	Human spliced tran	
C	85	21.4	0.9	48	19	AAV69937	Chlorella virus pr
C	86	21.4	0.9	48	24	AA521106	(GGA)16 DNA purifi
C	87	21.4	0.9	48	24	AAD24852	Chlorella virus cv
C	88	21.4	0.9	51	22	AA132465	Human SNP oligonuc
C	89	21.4	0.9	51	22	AA175865	Human silent SNP c
C	90	21.4	0.9	53	22	AAH93331	Plasmodium falcipar
C	91	21.4	0.9	59	21	AAAC11350	Human secreted prote
C	92	21.4	0.9	60	24	ABN32960	Human spliced tran
C	93	21.4	0.9	60	24	ABN37046	Human spliced tran
C	94	21.4	0.9	60	24	ABN37096	Human spliced tran
C	95	21.4	0.9	60	24	ABN50863	Human spliced tran
C	96	21.2	0.9	41	22	AAH44690	Human type-I amino
C	97	21.2	0.9	48	22	AAF29312	Primer base sequenc
C	98	21.2	0.9	50	22	AA177361	Human silent SNP c
C	99	21.2	0.9	51	21	AAAT7364	Human clone CG4491
C	100	21.2	0.9	51	22	AAH31990	Human SNP oligonuc

ALIGNMENTS

XX	RESULT 1
XX	ABEN1230
ID	ABEN41230 standard; DNA; 60 BP.
AC	ABEN41230;
XX	
DT	15-JUL-2002 (first entry)
XX	
DE	Human spliced transcript detection oligonucleotide SEQ ID NO:13978.
XX	
KW	Human; mouse; rat; splice transcript; detection; RNA transcript;
XX	
KW	splice variant; transcriptome; oligonucleotide library; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200210449-A2.
XX	
PD	07-FEB-2002.
XX	
PF	20-JUL-2001; 2001WO-IB01903.
XX	
PR	28-JUL-2000; 2000US-221607P.
XX	
PR	02-MAY-2001; 2001US-267724P.
XX	
PA	(COMP-) COMFUGEN INC.
XX	
PI	Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX	
DR	WPI; 2002-257383/30.
XX	
PT	New oligonucleotide libraries comprising oligonucleotides which
PT	selectively hybridize to mRNAs transcribed from a transcription unit of
PT	a genome, useful for detecting tissue-, pathology-, and
PT	developmental-specific genes
PS	
PS	Example 1; SEQ ID 13978; 47bp; English.
XX	
CC	The present invention describes oligonucleotide libraries for detecting
CC	messenger RNAs that populate a (sub-)transcriptome, where the
CC	(sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC	transcription units that populate a genome. The library comprises
CC	several oligonucleotides, each capable of hybridising selectively to a
CC	set of messenger RNAs transcribed from a given transcription unit of
CC	the genome, which encodes one or more messenger RNA splice variants.
CC	The oligonucleotide libraries are useful for detecting mRNAs from a
CC	biological sample, in expression profiling studies, in qualitatively or
CC	quantitatively characterising the corresponding transcriptome, and in
CC	detecting RNA transcripts and splice variants of human or animal
CC	transcriptomes. The libraries may also be used as specialised mini
CC	libraries to detect transcripts of a sub-transcriptome under a

CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 60 BP; 20 A; 12 C; 18 G; 10 T; 0 other;

Query Match 2.6%; Score 60; DB 24; Length 60;
Best Local Similarity 100.0%; Pred. No. 9,4e-06;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Gy 1468 ATAGGACGATGGATGTGACATGATGTTGGGGAAGCATCGGCACCATTTCATATGACAG 1527
Db 1 ATAGGACGATGGATGTGACATGATGTTGGGGAAGCATCGGCACCATTTCATATGACAG 60
|||||
|||

RESULT 2
ID AL28838/c
ID AL28838 standard; DNA; 51 BP.
AC
XX AAL28838;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #2046.

XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.

OS
XX Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PE 28-DEC-2000; 2000WO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
PR 27-DEC-2000; 2000US-0173419.
XX
PPA (CURA-) CURAGEN CORP.
PI Shimkets RA, Leach M;
PI WPI; 2001-465210/50.
DR
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer; autoimmune diseases and infections -
PT
PS Claim 1; Page 1966; 4143pp; English.
XX
XX The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptotic related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of

CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.

SO Sequence 51 BP; 12 A; 9 C; 9 G; 21 T; 0 other;

Query Match 2.2%; Score 51; DB 22; Length 51;
 Best Local Similarity 100.0%; Pred. No. 0.0018;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1707 TCATGTCATTACATACACCTTCGACACAGCAAAATTAACGTCGATT 1757
 DB 51 TCATGTCATTACATACACCTTCGACACAGCAAAATTAACGTCGATT 1

RESULT 3

AAI28841/c
 ID AAI28841 standard; DNA; 50 BP.

AAI28841;

24-JAN-2002 (first entry)

Human SNP oligonucleotide #2049.

Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;
 amyloid protein; angiotensin; apoptosis related protein; cadherin;
 cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 complement related protein; cytochrome; kinesin; cytokine; interferon;
 interleukin; G-protein coupled receptor; thioesterase; inflammation;
 multifactorial disease; autoimmune disease; infection;
 nervous system disease; ss.

OS Homo sapiens

PN WO200147944-A2.

PD 05-JUL-2001

PF 28-DEC-2000; 2000MO-US35498.

PR 28-DEC-1999; 99US-0173419.

PI 27-DEC-2000; 2000US-0173419.

PA (CURA-) CURAGEN CORP.

PI Shimketa RA, Leach M;

DR WPI; 2001-465210/50.

PT Polymorphic nucleic acids encoding e.g. amyases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -

PS Claim 1; Page 1967; 4143pp; English.

CC The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amyases, amyloid proteins, angiotensin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
 CC G-protein coupled receptors and thioesterases. The present sequence is
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded
 CC by them may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune

CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.

SO Sequence 50 BP; 13 A; 17 C; 3 G; 17 T; 0 other;

Query Match 2.1%; Score 50; DB 22; Length 50;
 Best Local Similarity 100.0%; Pred. No. 0.0033;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1610 GCATGCTTTTAAATGATTTAAGCAAAAGGTGAGAGGAGATGTGTG 1659
 DB 50 GCATGCTTTTAAATGATTTAAGCAAAAGGTGAGAGGAGATGTGTG 1

RESULT 4

AAI28839/c
 ID AAI28839 standard; DNA; 51 BP.

AAI28839;

24-JAN-2002 (first entry)

Human SNP oligonucleotide #2047.

Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;
 amyloid protein; angiotensin; apoptosis related protein; cadherin;
 cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 complement related protein; cytochrome; kinesin; cytokine; interferon;
 interleukin; G-protein coupled receptor; thioesterase; inflammation;
 multifactorial disease; autoimmune disease; infection;
 nervous system disease; ss.

OS Homo sapiens

PN WO200147944-A2.

PD 05-JUL-2001

PF 28-DEC-2000; 2000MO-US35498.

PR 28-DEC-1999; 99US-0173419.

PI 27-DEC-2000; 2000US-0173419.

PA (CURA-) CURAGEN CORP.

PI Shimketa RA, Leach M;

DR WPI; 2001-465210/50.

PT Polymorphic nucleic acids encoding e.g. amyases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -

PS Claim 1; Page 1966; 4143pp; English.

CC The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amyases, amyloid proteins, angiotensin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
 CC G-protein coupled receptors and thioesterases. The present sequence is
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded
 CC by them may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,

CC Leukemia), diseases of the nervous system and an infection of pathogenic
CC organisms.
SQ Sequence 51 BP, 10 A; 14 C; 9 G; 18 T; 0 other;
XX
Query Match 1.7%; Score 40; DB 22; Length 51;
Best Local Similarity 98.1%; Pred. No. 1.3;
Matches 51; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1655 GTGTGAGCATCTCTGCAAGGTGAACAAGACTCAAAATGACAGTTTCAGAGAG 1706
DB 51 GTGTGAGCATCTCTGCAAGGTGAACAAGACTCAAAATGACAGTTTCAGAGAG 1
RESULT 5
AAL28840/c
ID AAL28840 standard; DNA; 51 BP.
XX
AC AAL28840;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #2048.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cyostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000MO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
PR 27-DEC-2000; 2000US-0173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkete RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -
XX
PS Claim 1; Page 1967; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid protein, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukin,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukemia), diseases of the nervous system and an infection of pathogenic
CC organisms.
XX

SQ Sequence 51 BP, 10 A; 14 C; 9 G; 18 T; 0 other;
XX
Query Match 1.7%; Score 40; DB 22; Length 51;
Best Local Similarity 98.1%; Pred. No. 1.3;
Matches 51; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1655 GTGTGAGCATCTCTGCAAGGTGAACAAGACTCAAAATGACAGTTTCAGAGAG 1706
DB 51 GTGTGAGCATCTCTGCAAGGTGAACAAGACTCAAAATGACAGTTTCAGAGAG 1
RESULT 6
AAL29715/c
ID AAL29715 standard; DNA; 51 BP.
XX
AC AAL29715;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #2923.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cyostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000MO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
PR 27-DEC-2000; 2000US-0173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkete RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -
XX
PS Claim 1; Page 2223; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid protein, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukin,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukemia), diseases of the nervous system and an infection of pathogenic
CC organisms.
XX
SQ Sequence 51 BP, 8 A; 7 C; 3 G; 33 T; 0 other;
XX
Query Match 1.1%; Score 26.2; DB 22; Length 51;
XX

CC include are the encoding polynucleotides. The novel kinase is useful for
CC identifying a substance that modulates the activity of a kinase
CC The polynucleotide is useful for detecting nucleic acid encoding a kinase
CC polypeptide in a sample. The kinases, polynucleotides modulators
CC of the kinases and anti-kinase antibodies are useful for diagnosing and
CC treating a disease or disorder such as cancer, immune-related disease
CC and disorders, cardiovascular disease, brain or neuronal-associated
CC diseases, and metabolic disorders, e.g. cancers of tissues, cancers of
CC hematopoietic origin, diseases of the central or peripheral nervous
CC system, Alzheimer's disease, Parkinson's disease, multiple sclerosis,
CC amyotrophic lateral sclerosis, viral infections, infections caused by
CC prions, infections caused by bacteria, infections caused by fungi, or
CC ocular diseases, migraine, pain, sexual dysfunction, mood disorders,
CC attention disorders, cognition disorders, hypertension, hyperkalemia,
CC psychotic disorders, neurological disorders, dyskinesias, metabolic
CC disorders, or organ transplant rejection and many other diseases
CC and disorders given in the specification. The polynucleotide is
CC useful in gene therapy techniques. The two novel kinases are
CC designated SGK31 (the gene is located on chromosome Xp22.1) and SGK351
CC (chromosome 17q22-25). The present sequence is a PCR primer used to
CC investigate the tissue specific expression of SGK351.

XX SQ Sequence 25 BP, 6 A, 6 C, 5 G, 8 T, 0 other;

Query Match 1.1%; Score 25; DB 23; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1087 CACCTTAAGTGGGAGAACTTCTGG 1111
DB 25 CACCTTAAGTGGGAGAACTTCTGG 1

RESULT 11

ABNS9017
ID ABNS9017 standard; DNA; 60 BP.

AC ABNS9017;

XX 15-JUL-2002 (first entry)

DE Human spliced transcript detection oligonucleotide SEQ ID NO:31765.

XX Human; mouse; rat; splice transcript; detection; RNA transcript;

KM splice variant; transcriptome; oligonucleotide library; ss.

XX Homo sapiens.

XX MO200210449-A2.

XX 07-FEB-2002.

XX 20-JUL-2001; 2001WO-IB01903.

XX 28-JUL-2001; 2000US-221607P.

XX 02-MAY-2001; 2001US-287724P.

XX (COMP-) COMEUGEN INC.

XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S,

XX WPI; 2002-257383/30.

XX New oligonucleotide libraries comprising oligonucleotides which
XX selectively hybridize to mRNAs transcribed from a transcription unit of
XX a genome, useful for detecting tissue-, pathology-, and
XX developmental-specific genes

XX Example 1; SEQ ID 31765; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the
XX (sub-)transcriptome comprises messenger RNAs transcribed from multiple

CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridizing selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialized mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABNS5589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.

CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 60 BP, 9 A, 14 C, 14 G, 23 T, 0 other;

Query Match 1.0%; Score 24.4; DB 24; Length 60;
Best Local Similarity 68.0%; Pred. No. 1.5e+04;
Matches 34; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1223 CTCTCAGTGAAGTGGCAATGAGTCTTTCTGGGTTTACATATGAGCT 1272
DB 11 CACCTAGCTGAATGCAATGAGTCTTTCTGGGTTTACATATGAGCT 60

RESULT 12

AAV76048
ID AAV76048 standard; DNA; 57 BP.

AC AAV76048;

XX 16-MAR-1999 (first entry)

DE Staphylococcus aureus contig SEQ ID #1737.

XX Computer readable medium; vaccine; S.aureus infection; immunodetection;

KM cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;

KM skin infection; surgical wound infection; scalded skin syndrome;

XX toxic shock syndrome; ds.

XX Staphylococcus aureus.

XX EP786519-A2.

XX 30-JUL-1997.

XX 07-JAN-1997; 97EP-0100117.

XX 05-JAN-1996; 96US-0009861.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;

XX PI Rosen CA;

XX WPI; 1997-374922/35.

XX Polynucleotide(s) and proteins derived from Staphylococcus aureus
XX stored on computer readable medium and used in the production of
XX anti-S.aureus vaccines

XX Claim 1; Page 2046; 3271pp; English.

XX This sequence represents one of 5191 Staphylococcus aureus DNA sequences
XX of the invention. The DNA sequences are recorded on a computer readable

CC medium, preferably selected from a floppy or hard disk, random access
CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
CC the S.aureus DNA sequences allows putative functions to be assigned so
CC that protein-encoding or regulatory regions of commercial, therapeutic or
CC industrial importance can be obtained. Specifically, sequences which are
CC likely to encode antigens have been identified and these polypeptides can
CC be used in a vaccine composition against S.aureus infection. The
CC polypeptides can also be used in a kit for the immunodetection of
CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,
CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
CC skin and surgical wound infections, scalded skin syndrome, toxic shock
CC syndrome, etc. Organisms transformed with the DNA sequences can be used
CC for recombinant production of the polypeptides. The new DNA sequences
CC (and their fragments) are useful as primers or probes for isolating
CC homologues of any of the S.aureus DNA sequences contained on the
CC computer readable medium.

XX SQ Sequence 57 BP; 29 A; 6 C; 10 G; 12 T; 0 other;

XX Query Match 1.0%; Score 24.2; DB 18; Length 57;
XX Best Local Similarity 71.1%; Pred. No. 1.6e+04;
XX Matches 32; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 421 AGAATGCTAAAGATACGCTCATACAAAGCAGACGAAATATT 465
DB 1 AAAGAGCTAAAGAAAGATGATTAACAGCAAAAGGATTATT 45

RESULT 13
AAT32212
ID AAT32212 standard; DNA; 30 BP.

XX XX AAT32212;

XX 26-SEP-1996 (first entry)

XX Rat mitogen-activated S6 kinase p70s6kdeltan PCR primer.

XX PCR primer; polymerase chain reaction; amplification; construction;
XX transcription system; measurement; interaction; phosphatase; kinase
XX auto-inhibitory domain; identification; antagonist; agonist;
XX calcineurin; inhibition; T-cell activation; prevention; cancer;
XX graft rejection; treatment; arthritis; autoimmune disease; allergy;
XX psoriasis; Alzheimer's disease; regulation; cell proliferation;
XX rat; mitogen-activated S6 kinase; ss.

XX OS Synthetic.

XX WO9603501-A1.

XX PD 08-FEB-1996.

XX PF 12-JUL-1995; 95WO-EP02724.

XX PR 22-JUL-1994; 94EP-0810435.

XX PA (CIBA) CIBA GEIGY AG.

XX PI Chaudhuri B, Furst P, Stephan C, Fuerst P;
XX WPI; 1996-117046/12.

XX Transcription system for measuring interaction between phosphatase
XX or kinase and its auto-inhibitory domain - used to identify agonist
XX or antagonists of kinase(s) useful e.g. in preventing graft
XX rejection

XX PS Example 16; Page 66; 83pp; English.

XX CC The primer pair AAT32210/12 was used for the PCR amplification of
XX the rat mitogen-activated S6 kinase, p70s6kdeltad. The PCR prod.
XX was used in the construction of a transcription system (TS), for
XX measuring interaction between a phosphatase or kinase (POK),

CC including muteins or fragments which bind an autoinhibitory domain
CC (AID), and an AID. The TS comprises the DNA binding domain (DBD)
CC of a transcription factor (TF), and separately the transcription
CC activation domain of a TF, where the domains are respectively
CC linked to a 1st polypeptide comprising a POK (or an AID binding
CC fragment), and a 2nd polypeptide comprising an AID able to bind
CC the 1st polypeptide. The TS can be used for the identification of
CC POK (antagonists, e.g. calcineurin (antagonists which can be
CC used inhibit T-cell activation, e.g. to prevent graft rejection.
CC Other possible applications of the (ant)agonists are in the
CC treatment of cancer, arthritis, psoriasis, autoimmune disease,
CC allergy and Alzheimer's disease, and in the regulation of cell
CC proliferation.

XX SQ Sequence 30 BP; 7 A; 5 C; 8 G; 10 T; 0 other;

XX Query Match 1.0%; Score 24; DB 17; Length 30;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+04;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 289 CCAGATGTTTGGAGCTACTTCGG 312
DB 7 CCAGATGTTTGGAGCTACTTCGG 30

RESULT 14
AAT32213
ID AAT32213 standard; DNA; 32 BP.

XX XX AAT32213;

XX 26-SEP-1996 (first entry)

XX Yeast ACE1-rat mitogen-activated S6 kinase fusion gene PCR primer.

XX PCR primer; polymerase chain reaction; amplification; construction;
XX transcription system; measurement; interaction; phosphatase; kinase
XX auto-inhibitory domain; identification; antagonist; agonist;
XX calcineurin; inhibition; T-cell activation; prevention; cancer;
XX graft rejection; treatment; arthritis; autoimmune disease; allergy;
XX psoriasis; Alzheimer's disease; regulation; cell proliferation;
XX rat; mitogen-activated S6 kinase; yeast; transcriptional activator;
XX fusion; ss.

XX OS Synthetic.

XX WO9603501-A1.

XX PD 08-FEB-1996.

XX PF 12-JUL-1995; 95WO-EP02724.

XX PR 22-JUL-1994; 94EP-0810435.

XX PA (CIBA) CIBA GEIGY AG.

XX PI Chaudhuri B, Furst P, Stephan C, Fuerst P;
XX WPI; 1996-117046/12.

XX Transcription system for measuring interaction between phosphatase
XX or kinase and its auto-inhibitory domain - used to identify agonist
XX or antagonists of kinase(s) useful e.g. in preventing graft
XX rejection

XX PS Example 17; Page 67; 83pp; English.

XX CC The primer pair AAT32210/13 was used for the PCR amplification of a
XX yeast transcriptional activator (ACE1)/rat mitogen-activated S6
XX kinase, fusion gene. The PCR prod. was used in the construction of
XX a transcription system (TS), for measuring interaction between a
XX phosphatase or kinase (POK), including muteins or fragments which
XX bind an autoinhibitory domain (AID), and an AID. The TS comprises

CC the DNA binding domain (DBD) of a transcription factor (TF), and
CC separately the transcription activation domain of a TF, where the
CC domains are respectively linked to a 1st polypeptide comprising a
CC Pok (or an AID binding fragment), and a 2nd polypeptide comprising
CC an AID able to bind the 1st polypeptide. The TS can be used for
CC the identification of Pok (ant)agonists, e.g. calcitriol
CC (ant)agonists which can be used inhibit T-cell activation, e.g. to
CC prevent graft rejection. Other possible applications of the
CC (ant)agonists are in the treatment of cancer, arthritis, psoriasis,
CC autoimmune disease, allergy and Alzheimer's disease, and in the
CC regulation of cell proliferation.

XX Sequence 32 BP; 12 A; 4 C; 5 G; 11 T; 0 other;

XX Query Match 1.0%; Score 23.8; DB 17; Length 32;

XX Best Local Similarity 92.6%; Pred. No. 1.6e+04; Mismatches 0; Gaps 0;

XX Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1290 TGTGAAAGAAAGTTTCCTTGACC 1316

DB 6 TGTGAAAGAAAGTTTCCTTGACC 32

RESULT 15 AAL29254/c

XX AAL29254 standard; DNA; 49 BP.

XX AAL29254;

XX 24-JUN-2002 (first entry)

XX Human SNP oligonucleotide #2462.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX neuroprotective; anticarcinogenic; gene therapy; vaccine; cancer;
XX amyloid protein; angiotensin; apoptosis related protein; cadherin;
XX cyclin; polymerase; histone; kinase; colony stimulating factor;
XX complement related protein; cytochrome; cytokine; interferon;
XX interleukin; G-protein coupled receptor; thioesterase; inflammation;
XX multifactorial disease; autoimmune disease; infection;
XX nervous system disease; ss.

XX Homo sapiens.

XX WO200147944-A2.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000MO-US3498.

XX 28-DEC-1999; 99US-0173419.

XX 27-DEC-2000; 2000US-0173419.

XX (CURA-) CURAGEN CORP.

XX Shinketsu RA, Leach M;

XX WPI; 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX oncogenes and histones, useful for diagnosing and treating, e.g.
XX cancer, autoimmune diseases and infections -
XX Claim 1; Page 2088; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic
XX variants of proteins related to amylases, amyloid proteins, angiotensin,
XX apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
XX histones, kinases, colony stimulating factors, complement related
XX proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
XX G-protein coupled receptors and thioesterases. The present sequence is
XX one such oligonucleotide. The oligonucleotides and the peptides encoded
XX by them may be used in the prevention, diagnosis and treatment of

CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukemia), diseases of the nervous system and an infection of pathogenic
CC organisms.

XX Sequence 49 BP; 3 A; 3 C; 4 G; 39 T; 0 other;

XX Query Match 1.0%; Score 23.8; DB 22; Length 49;

XX Best Local Similarity 72.1%; Pred. No. 1.9e+04; Mismatches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1760 AAAAATCATCATGTCGAAAAAACTTAACCAATA 1802

DB 48 AAAAATCATCATGTCGCCCCAAAAAAATTAATA 6

RESULT 16

XX ABN45373/c

XX ABN45373 standard; DNA; 60 BP.

XX ABN45373;

XX 15-JUL-2002 (first entry)

XX Human spliced transcript detection oligonucleotide SEQ ID NO:18121.

XX Human; mouse; rat; splice transcript; detection; RNA transcript;

XX splice variant; transcriptome; oligonucleotide library; ss.

XX Homo sapiens.

XX WO200210449-A2.

XX 07-FEB-2002.

XX 20-JUL-2001; 2001MO-1B01903.

XX 28-JUL-2000; 2000US-221607P.

XX 02-MAY-2001; 2001US-287724P.

XX (COMP-) COMPUGEN INC.

XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX WPI; 2002-257383/30.

XX New oligonucleotide libraries comprising oligonucleotides which
XX selectively hybridize to mRNAs transcribed from a transcription unit of
XX a genome, useful for detecting tissue-, pathology-, and
XX developmental-specific genes
XX Example 1; SEQ ID 18121; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the
XX (sub-)transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises
XX several oligonucleotides, each capable of hybridizing selectively to a
XX set of messenger RNAs transcribed from a given transcription unit of
XX the genome, which encodes one or more messenger RNA splice variants.
XX The oligonucleotide libraries are useful for detecting mRNAs from a
XX biological sample, in expression profiling studies, in qualitatively or
XX quantitatively characterizing the corresponding transcriptome, and in
XX detecting RNA transcripts and splice variants of human or animal
XX transcriptomes. The libraries may also be used as specialised mini
XX libraries to detect transcripts of a sub-transcriptome under a
XX particular biological or pathological state, and so allowing the
XX detection of tissue- and pathology-specific genes such as those genes
XX only expressed in specific tissue under a specific pathological

CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 60 BP; 8 A; 10 C; 13 G; 29 T; 0 other;
XX
Query Match 1.0%; Score 23.8; DB 24; Length 60;
Best Local Similarity 62.7%; Pred. No. 2.1e+04;
Matches 37; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
XX
QY 246 AATTCGAAACTGTGTGACACAGAGCCCGAATAATCAGACAGATTTTGAGC 304
DB 59 AACGACAGACACTGTGTGAAACAAAGCAGTAAATTTGAGACCCAAATTTGACGC 1
XX
RESULT 17
ABN50683
ID ABN50683 standard; DNA; 60 BP.
XX
AC ABN50683;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:23431.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KM splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB01903.
XX
PR 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUTEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
PT WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes.
XX
PS Example 1; SEQ ID 23431; 47pp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the
XX (sub-)transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises
XX several oligonucleotides, each capable of hybridizing selectively to a
XX set of messenger RNAs transcribed from a given transcription unit of
XX the genome, which encodes one or more messenger RNA splice variants.
XX The oligonucleotide libraries are useful for detecting mRNAs from a
XX biological sample, in expression profiling studies, in qualitatively or
XX quantitatively characterizing the corresponding transcriptome, and in
XX detecting RNA transcripts and splice variants of human or animal
XX transcriptomes. The libraries may also be used as specialised mini
XX libraries to detect transcripts of a sub-transcriptome under a
XX particular biological or pathological state, and so allowing the
XX detection of tissue- and pathology-specific genes such as those genes
XX only expressed in specific tissue under a specific pathological

CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 60 BP; 19 A; 11 C; 17 G; 13 T; 0 other;
XX
Query Match 1.0%; Score 23.8; DB 24; Length 60;
Best Local Similarity 66.7%; Pred. No. 2.1e+04;
Matches 34; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
XX
QY 2180 TTTAAATGCGAAATATTGTGTGTGAGAAAGCAGACACTTCTCT 2230
DB 9 TTTACACTGTGCAGATTTTGTGAGAGAGTGCATTAAGACAGGAACTACTCT 59
XX
RESULT 18
ABL00050
ID ABL00050 standard; DNA; 50 BP.
XX
AC ABL00050;
XX
DT 05-MAR-2002 (first entry)
XX
DE Human silent noncoding SNP oligonucleotide SEQ ID NO:41.
XX
KW Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
KM immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;
KM autoimmune disease; inflammation; cancer; nervous system disease;
XX
XX infection; polymorphic protein; ds.
XX
OS Homo sapiens.
XX
PN WO200138586-A2.
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-US32311.
XX
PR 24-NOV-1999; 99US-0167383.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
PT WPI; 2001-355949/37.
XX
PT Isolated human nucleic acids comprising one or more single nucleotide
PT polymorphisms, useful for treating a subject suffering from a
PT pathology, e.g. autoimmune diseases, ascribed to the presence of a
PT sequence polymorphism.
XX
PS Claim 1; Page 257; 674pp; English.
XX
XX ABL00010 to ABL01104 represent human nucleic acid oligonucleotides
XX comprising one or more single nucleotide polymorphisms (SNPs). ABB56531
XX to ABB56903 represent human peptides encoded by some of the SNP
XX oligonucleotides. The sequences from the present invention can have
XX immunosuppressive, cytostatic, antiinflammatory, neuroprotective and
XX antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides
XX and antibodies from the present invention can be used for treating a
XX subject suffering from, at risk for, or suspected of, suffering from a
XX pathology ascribed to the presence of a sequence polymorphism. The
XX pathology may be autoimmune diseases, inflammation, cancer, diseases of
XX the nervous system, and infection by pathogenic microorganisms. The SNPs
XX are also useful for determining which forms of a characterised
XX polymorphism are present in individuals. The antibodies may be used in
XX the detection, quantitation and/or cellular or tissue localisation of a
XX polymorphic protein (e.g., for use in measuring levels of the

CC polymorphic protein within appropriate physiological samples).

SQ Sequence 50 BP; 22 A; 5 C; 3 G; 20 T; 0 other;

Query Match 1.0%; Score 23.6; DB 23; Length 50;

Best Local Similarity 76.3%; Pred. No. 2.2e+04; Matches 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2117 TATATTAATATATATTTTTCATAATAGATTTTGGATTCA 2154

DB 13 TATATATATATATTTTATCCAAAAATATGTTTATACA 50

RESULT 19

AAI28430/c

AAI28430 standard; DNA; 51 BP.

AAI28430;

24-JAN-2002 (first entry)

Human SNP oligonucleotide #1638.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
XX amyloid protein; angiotensin; apoptosis related protein; cadherin;
XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
XX complement related protein; cytochrome; kinesin; cytokine; interferon;
XX interleukin; G-protein coupled receptor; cholestase; inflammation;
XX multifactorial disease; autoimmune disease; infection;
XX nervous system disease; ss.

OS Homo sapiens.

XX MO200147944-A2.

PN 05-JUL-2001.

28-DEC-2000; 2000MO-US35498.

28-DEC-1999; 99US-0173419.

27-DEC-2000; 2000US-0173419.

(CURA-) CURAGEN CORP.

Shinkets RA, Leach M;

WPI; 2001-465210/50.

Polymorphic nucleic acids encoding e.g. amyloses, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections -

Claim 1; Page 1849; 4143pp; English.

The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amyloses, amyloid proteins, angiotensin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and cholestases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney leukemia), diseases of the nervous system and an infection of pathogenic organisms.

Sequence 51 BP; 8 A; 2 C; 1 G; 40 T; 0 other;

Query Match 1.0%; Score 23.6; DB 22; Length 51;

Best Local Similarity 69.6%; Pred. No. 2.2e+04; Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1757 TTTTAAAAATCATTCATGTCGCAAAAAAACTTAAGCAAAATA 1802

DB 51 TTTTAAAAATMAAACATTTGATMAAAGMAAAAAAAAAAAAAA 6

RESULT 20

AAH84250

AAH84250 standard; cDNA; 60 BP.

AAH84250;

21-SEP-2001 (first entry)

Human cell death protective cDNA clone CNI-00717 ORF24, SEQ:231.

XX Cell death protective; apoptosis; necrosis; human; drug screening;
XX cell death-associated disorder; central nervous system disorder;
XX psychiatric disorder; neurological disorder; ischaemia-related disorder;
XX stroke; cerebral infarction; ischaemic encephalopathy;
XX neurodegenerative disorder; Alzheimer's disease; Huntington's disease;
XX Parkinson's disease; infection; meningitis; malaria; trypanosomiasis;
XX vascular disease; ophthalmological disorder; diabetic retinopathy;
XX macular degeneration; hypertension; myocardial infarction;
XX atherosclerosis; respiratory disorder; asthma; transgenic animal;
XX chronic obstructive pulmonary disease; neoplastic condition; cancer;
XX benign tumour; anaemia; gastrointestinal disorder; gastritis;
XX ulcerative colitis; liver disease; biliary cirrhosis; kidney disorder;
XX glomerulonephritis; cystitis; endometriosis; endocrine disorder;
XX Grave's disease; Hashimoto's thyroiditis; skin condition; dermatitis;
XX urticaria; immune disorder; acquired immunodeficiency syndrome; AIDS;
XX open reading frame; ORF; ss.

OS Homo sapiens.

XX MO200145638-A2.

PN 28-JUN-2001.

11-DEC-2000; 2000MO-US33547.

14-DEC-1999; 99US-0461697.

(COGE-) COGENT NEUROSCIENCE INC.

Lo DC, Barney S, Thomas MB, Portbury SD, Puranam K, Katz LC;

WPI; 2001-390297/41.

P-PsDB; AAG98720.

Novel protective sequence polymucleotides and polypeptides, used to identify modulators of their expression and activity, which are used in to treat central nervous system conditions, diseases and disorders -

Claim 2; Fig 9X; 325pp; English.

Sequences AAH84132-AAH84170 represent human nucleic acid sequences which protect against cell death (i.e., apoptosis or necrosis). Sequences AAH84132, AAH84145, AAH84170, AAH84201, AAH84210, AAH84226, AAH84265, AAH84281, AAH84315 and AAH84367 represent 10 full-length cDNA clones, while the remaining nucleic acid sequences within the range given above represent the open reading frames (ORFs) of these cDNA clones. Sequences AAAG9610-AAAG9829 represent the polypeptides encoded by the cell death protective ORFs. The cell death protective cDNA clones are able to prevent, delay or reverse progression through the apoptotic or necrotic pathways when injected into a cell predisposed to or undergoing cell death. The cell death protective nucleic acids and polypeptides can be used in the diagnosis and treatment of disorders associated with cell death, and to screen for compounds which modulate their activity or

expression. Such modulators, preferably a small organic molecule, an antibody, a ribozyme, or an antisense molecule, can also be used to treat cell death-related diseases. Such diseases include those associated with the central nervous system including psychiatric or neurological disorders, especially ischaemia-related conditions such as strokes, and also includes neurodegenerative disorders such as Alzheimer's disease, Huntington's disease, or Parkinson's disease. The modulators may also be used to treat infectious diseases such as meningitis, malaria, or trypanosomiasis; vascular diseases such as ischaemic encephalopathy or cerebral infarction; eye conditions such as diabetic retinopathy or macular degeneration; hypertension; myocardial infarction; atherosclerosis; respiratory conditions such as asthma or chronic obstructive pulmonary disease; neoplastic conditions such as cancers or benign tumours; blood cell conditions such as anaemia; gastrointestinal conditions such as gastritis or ulcerative colitis; liver conditions such as biliary cirrhosis; kidney disorders such as glomerulonephritis; cystitis; endometriosis; endocrine disorders such as Graves' disease or Hashimoto's thyroiditis; skin conditions such as dermatitis or urticaria; or immune system disorders such as acquired immunodeficiency syndrome (AIDS). The nucleic acids may additionally be used to generate animal models of cell death-associated disorders. The present sequence represents a cell death protective ORF.

XX Sequence 60 BP, 31 A, 1 C, 20 G, 8 T, 0 other;

Query Match 1.0%; Score 23.6; DB 22; Length 60;
Best Local Similarity 64.8%; Pred.No. 2.4e+04;
Matches 35; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1635 AAAAAAGTGGAGAGGAGATGTGTGAGCATCTGCAAGCTGMAAACAACACCA 1668
DB 7 AAGAGAGATGAAAGTGGAAATGAGMAAGCTGMAAAGAGMAAGATTAA 60

RESULT 21

AA519340 standard; DNA, 58 BP.

XX AAS19340;

XX 20-MAR-2002 (first entry)

XX Oligonucleotide 5981 used to construct plasmid XL2725.

XX ss; DNA purification; triple helix; plasmid purification;

KW Oligonucleotide 5981; XL2725.

XX Synthetic.

XX Key Location/Qualifiers

XX Repeat_region

XX repeat_unit

XX repeat_unit

XX repeat_unit

XX repeat_unit

XX repeat_unit

XX repeat_unit

XX repeat_unit

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XX repeat_unit

XX repeat_unit

PT comprising a covalently coupled oligonucleotide able to form a triple
XX helix with the dsDNA
XX Example 7.1; Page 20; 40pp; English.

XX This invention comprises a method of purifying double-stranded DNA from
CC a solution containing the double-stranded DNA mixed with other
CC components, comprising passing the solution through a support comprising
CC a covalently coupled oligonucleotide capable of forming a triple helix
CC with the double-stranded DNA by hybridisation with a specific sequence
CC present in the double-stranded DNA. The method is useful for purifying
CC double-stranded DNA contained in a solution and mixed with other
CC components. The new method is a simple, rapid and effective method for
CC DNA purification, and makes it possible to obtain especially high
CC purities with high yields. The method enables DNA to be purified from
CC complex mixtures comprising other nucleic acids, proteins, endotoxins,
CC nucleases and the like. The supports may be readily recycled, and the
CC DNAs obtained display improved properties to pharmaceutical safety.
CC Further, the method entails only one step contrary to prior art.
CC The present sequence represents an oligonucleotide 5981 used to
CC create the XL2725 plasmid which was used in an example of the DNA
CC purification method of the invention.

XX Sequence 58 BP, 18 A, 2 C, 37 G, 1 T, 0 other;

Query Match 1.0%; Score 23.4; DB 24; Length 58;
Best Local Similarity 63.2%; Pred.No. 2.7e+04;
Matches 36; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 118 GACTGACCAACGACGAGAGCGGCGCTGAGAGTACGTGAGAGGAGGGGCTCAG 174
DB 1 GATCCGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAG 57

RESULT 22

AA22872/c standard; cDNA to mRNA, 50 BP.

XX AAT22872;

XX 29-AUG-1996 (first entry)

XX Human gene signature HUMGS04557.

XX Gene signature; messenger RNA; mRNA; relative abundance; frequency;

KW human; cloning; mapping; non-biased library; diagnosis; detection;

XX cell typing; abnormal cell function; ss.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

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XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

Claim 1; Page 1231; 2245pp; Japanese.
A single-stranded DNA (or its complementary strand or the corresp.

CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amyloses, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,

CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interleukins, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of

CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney, leukemia),
CC diseases of the nervous system and an infection of pathogenic
CC organisms.
XX
SQ Sequence 51 BP; 5 A; 4 C; 4 G; 38 T; 0 other;
XX
Query Match 1.0%; Score 23.2; DB 22; Length 51;
Best Local Similarity 70.5%; Pred. No. 2.8e+04;
Matches 31; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
XX
Qy 1759 TAAATAATCATCATGTGCAAAAAAACTTAAGCAATA 1802
Db 45 TAAATAATCATGTGCAAAAAAACTTAAGCAATA 2
XX
RESULT 25
ID AEN34677 standard; DNA; 60 BP.
XX
AC AEN34677;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:7425.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
XX splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB01903.
XX
PR 28-JUL-2000; 2000US-221607P.
XX 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
XX selectively hybridize to mRNAs transcribed from a transcription unit of
XX a genome, useful for detecting tissue-, pathology-, and
XX developmental-specific genes -
XX
PS Example 1; SEQ ID 7425; 47bp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the
XX (sub-)transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises
XX several oligonucleotides, each capable of hybridizing selectively to a
XX set of messenger RNAs transcribed from a given transcription unit of
XX the genome, which encodes one or more messenger RNA splice variants.
XX The oligonucleotide libraries are useful for detecting mRNAs from a
XX biological sample, in expression profiling studies, in qualitatively or
XX quantitatively characterizing the corresponding transcriptome, and in
XX detecting RNA transcripts and splice variants of human or animal
XX transcriptomes. The libraries may also be used as specialised mini
XX libraries to detect transcripts of a sub-transcriptome under a
XX particular biological or pathological state, and so allowing the
XX detection of tissue- and pathology-specific genes such as those
XX only expressed in specific tissue under a specific pathological

CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. AEN27253 to AEN35589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 60 BP; 17 A; 19 C; 11 G; 13 T; 0 other;
XX
Query Match 1.0%; Score 23.2; DB 24; Length 60;
Best Local Similarity 65.4%; Pred. No. 3.1e+04;
Matches 34; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
XX
Qy 1538 GGCCATACAAAAACAAGCTTTCCCATGATCTCAACGCGAGACACT 1589
Db 5 GGAGCTCAAAAGCTCTAGCCTTGCCGAGCTTCTTCAATCAGACCCCT 56
XX
RESULT 26
ID AAH44691/c
XX
AC AAH44691;
XX
DT 07-DEC-2001 (first entry)
XX
DE Human type-I aminoacyl tRNA synthetase 10 probe 2 SEQ ID NO:9.
XX
KW Human; type-I aminoacyl tRNA synthetase 10; malignant tumour;
XX hemopathy; human immunodeficiency virus; HIV infection;
XX immunological disease; inflammation; probe; ss.
XX
OS Homo sapiens.
XX
PN CN1301715-A.
XX
PD 04-JUL-2001.
XX
PF 27-DEC-1999; 99CN-0125371.
XX
PR 27-DEC-1999; 99CN-0125371.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2001-550469/62.
XX
PT New polypeptide-I-type aminoacyl tRNA synthetase 10 and encoding
XX polynucleotide useful for treating tumor, hemopathy, infection and
XX immunological disease -
XX
PS Example 7; Page 20 (Disclosure); 32bp; Chinese.
XX
CC The present invention describes the human type-I aminoacyl tRNA
XX synthetase 10 protein. Also described are polynucleotides encoding the
XX type-I amino acyl tRNA synthetase 10 protein, and a DNA recombination
XX process to produce the protein. The protein can be used for treating
XX various diseases, such as malignant tumour, haemopathy, human
XX immunodeficiency virus infection, immunological diseases and various
XX inflammations. The present sequence represents a probe for type-I
XX aminoacyl tRNA synthetase 10, which is used in an example from the
XX present invention.
XX
SQ Sequence 41 BP; 3 A; 5 C; 4 G; 29 T; 0 other;
XX
Query Match 1.0%; Score 22.8; DB 22; Length 41;
Best Local Similarity 79.4%; Pred. No. 3.2e+04;
Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
XX
Qy 2045 AAAATGGAGGCAAGACAAAGAACTTACCA 2078

XX	MO200147944-A2.
XX	05-JUL-2001.
PD	
PF	28-DEC-2000; 2000WO-US35498.
XX	
PR	28-DEC-1999; 99US-0173419.
PR	27-DEC-2000; 2000US-0173419.
PA	(CUPRA-) CUPAGEN CORP.
XX	
P1	Shinkets RA, Leach M;
XX	
DR	WPI; 2001-465210/50.
PT	
PT	polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PS	cancers, autoimmune diseases and infections -
XX	
XX	Claim 1; Page 2908; 4143pp; English.
CC	The present invention relates to oligonucleotides encoding polymorphic
CC	variants of proteins related to amylases, amyloid proteins, angiotensin,
CC	apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC	histones, kinases, colony stimulating factors, complement related
CC	proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC	G-protein coupled receptors and thioesterases. The present sequence is
CC	one such oligonucleotide. The oligonucleotides and the peptides encoded
CC	by them may be used in the prevention, diagnosis and treatment of
CC	diseases associated with inappropriate expression of the proteins listed
CC	above. Disorders that may be prevented, diagnosed and/or treated include
CC	multifactorial diseases with a genetic component, such as autoimmune
CC	diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC	systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC	(e.g. cancers of the bladder, brain, breast, colon and kidney,
CC	leukaemia), diseases of the nervous system and an infection of pathogenic
CC	organisms.
SQ	
XX	Sequence 51 BP; 17 A; 5 C; 5 G; 24 T; 0 other;
Query Match	1.0%; Score 22.8; DB 22; Length 51;
Best Local Similarity	71.4%; Pred. No. 3.6e+04;
Matches 30; Conservative	0; Mismatches 12; Indels 0; Gaps 0
DY	2120 ATTAATATATATTTCATAATGATTTTGGATTCAGCTCATTT 2161
Db	7 AGAAGAATTTTTTTTCAGATGATTTTGAAACTTTTATT 48
RESULT 32	
AAC78364/C	
ID	AAC78364 standard, cDNA, 60 BP.
XX	
AC	AAC78364;
XX	
DT	08-FEB-2001 (first entry)
DE	
XX	
XX	Human cancer associated gene sequence SEQ ID NO:758.
KM	Human, cancer associated gene, cancer antigen, detection, cancer;
KM	diagnosis, cytostatic; proliferative; vulnerable; immunomodulator;
KM	antidiabetic; antineoplastic; antiatherosclerotic; antiviral;
KM	antiinflammatory; antihypertensive; antibacterial; cardiac;
KM	dematological; neuroprotective; thrombolytic; coagulant; neotropic;
KM	vasoconstrictor; antiproliferative; angiogenesis; gene therapy; inflammation;
KM	immune disorder; haematopoietic cell disorder; autoimmune disorder;
KM	allergic reaction; graft versus host disease; organ rejection;
KM	haemostatic; thrombolytic; cardiovascular disorder; infection;
XX	neurological disease; drug screening; ss.
OS	Homo sapiens.
XX	
XX	WO200055350-A1.

PD	21-SEP-2000.
XX	
PF	08-MAR-2000; 2000OWO-US05882.
XX	
PR	12-MAR-1999; 99US-0124270.
XX	
PA	(HUMA-) HUMAN GENOME SCL INC.
XX	
P1	Rosen CA, Ruben SM;
DR	WPI; 2000-587533/55.
DR	P-PSDB; AAB44155.
XX	
PT	Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer -
XX	
PS	Claim 1; Page 1305; 2352pp; English.
XX	
CC	AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44233. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerability; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antixanthitic; antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral; dermatological; neuroprotective; cardiact; thrombolytic; coagulant; neotrophic; vasotropic; antipsoriatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of the present invention.
CC	
CC	
CC	Sequence 60 BP; 10 A; 2 C; 5 G; 38 T; 5 other;
SQ	
Query Match	1.0%; Score 22.8; DB 21; Length 60;
Best Local Similarity	63.8%; Pred. No. 3.9e+04;
Matches 30; Conservative	0; Mismatches 17; Indels 0; Gaps 0;
CY	1756 TTTTAAATAATCAATCATGTGCGAAAAAACAATTAGCAATA 1802 ID TTTTAAAANNAANNAANNAANNAANNAANNAANNAANNAANNA 10
Db	56
RESULT 33	
AAZ6546/c	
ID	AAZ6546 standard; DNA; 47 BP.
XX	
XX	AAZ6546;
DT	10-SEP-2001 (first entry)
DE	Human map-related biallelic marker SEQ ID NO:893.
XX	
XX	Human genome, biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haployping; hybridisation; identification; characterisation; diagnosis; single nucleotide polymorphism; SNP; ds.
KM	
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Variation replace(24,G)
FT	/tag= a
FT	/standard_name= "single nucleotide polymorphism"

PA (ORCH-) ORCHID BIOSCIENCES INC.
 XX Picoult-Newburg L, Pohl M;
 XX WPI; 2001-290930/30.
 DR WPI; 2001-290930/30.
 XX New genotyping oligonucleotide, useful for detecting the presence,
 PT absence or identity of single polynucleotide polymorphism in a nucleic
 PT acid sample -
 XX
 PS Claim 1; Page 55; 83pp; English.
 XX
 CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
 CC primer extension (SNPE) primers, and the sequences of regions flanking
 CC sites of single nucleotide polymorphisms SNPs. The present invention
 CC includes kits for determining the presence or absence of a SNP, using the
 CC oligonucleotides of the invention. The PCR primers are used to amplify a
 CC SNP flanking sequence, the SNPs primer is used as a genotyping primer.
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by
 CC performing a single-nucleotide primer extension reaction. The
 CC oligonucleotides are useful for determining the presence, absence or
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
 CC assess by association analysis the genotype of an individual or group of
 CC individuals, having a pathological phenotypic trait suspected of being
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
 CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
 CC dystrophy, familial hypercholesterolemia, polycystic kidney disease,
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
 CC traits also include symptoms of or susceptibility to multifactorial
 CC disease of which a component is or may be genetic such as autoimmune
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,
 CC inflammation, cancer, nervous system diseases and infection by pathogenic
 CC microorganism. The method is also useful in forensic investigations and
 CC paternity analysis. The present sequence represents a fragment of human
 CC DNA flanking the site of a single nucleotide polymorphism.
 XX
 SQ Sequence 51 BP; 13 A; 9 C; 8 G; 20 T; 1 other;
 Query Match 1.0%; Score 22.6; DB 22; Length 51;
 Best Local Similarity 68.9%; Pred. No. 4e+04;
 Matches 31; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
 QY 406 AAGGCATGATAGTAAAGATGCTTAAGATACAGCTCATACAAA 450
 DB 51 ATGGCATGATATTCAGACACATACAGATATCTCTGTAATAA 7
 RESULT 36
 AAV65911
 ID AAV65911 standard; DNA; 54 BP.
 AC AAV65911;
 XX
 XX 02-FEB-1999 (first entry)
 DT
 XX
 XX HCMV target DNA for invasive cleavage.
 DE
 XX Nucleic acid detection; multiple sequential invasive cleavage;
 KW Invader-directed cleavage assay; nuclease; FEN-1; HCMV; ss.
 XX
 XX Human cytomegalovirus.
 OS
 XX
 PN MO9842873-A1.
 XX
 XX 01-OCT-1998.
 PD
 XX
 XX 24-MAR-1998; 98WO-US05809.
 PF
 XX
 XX 24-MAR-1997; 97US-0823516.
 PR
 XX
 XX (THIR-) THIRD WAVE TECHNOLOGIES INC.
 PA
 XX Brow MAD, Hall JG, Kwiatkowski RW, Lyamlichev VI;

PI Mast AL, VAVIA SH;
 XX
 XX WPI; 1998-557036/47.
 DR
 XX
 XX Detecting target nucleic acid by sequence-specific cleavage of
 PT complex with two specific oligonucleotides - used to detect
 PT cytomegalovirus DNA
 PT
 XX
 PS Example 48; Page 358; 524pp; English.
 XX
 CC This nucleotide sequence corresponds to nucleotides 3057-3110 of
 CC human cytomegalovirus (HCMV) genomic DNA. It was used as a target
 CC to demonstrate invasive cleavage using Invader oligonucleotide
 CC 89-44 (AAV65909), fluorescein-labelled probe 89-76 (see AAV65910) and
 CC FEN-1 nuclease (see AAV79970). The invader-directed cleavage
 CC reaction and the sequential invader-directed cleavage reaction of
 CC the present invention provide direct detection methods that combine
 CC the advantages of direct detection assays with the specificity
 CC provided by a dual or tri oligonucleotide hybridisation assay. The
 CC invention relates to means for the detection and characterisation
 CC of nucleic acid sequences, and variations in nucleic acid sequences.
 XX
 SQ Sequence 54 BP; 14 A; 7 C; 25 G; 8 T; 0 other;
 Query Match 1.0%; Score 22.6; DB 19; Length 54;
 Best Local Similarity 75.7%; Pred. No. 4.2e+04;
 Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 128 AGCCAGAGAGCGGGCTCTGAGGATGAGCTGAGGA 164
 DB 4 AGGAGAGGAGGAGGAGGCTCAAGAGAGCGGAGGA 40
 RESULT 37
 AEN35460
 ID AEN35460 standard; DNA; 60 BP.
 XX
 XX AEN35460;
 AC
 XX
 XX 15-UTL-2002 (first entry)
 DT
 XX
 XX Human spliced transcript detection oligonucleotide SEQ ID NO:8208.
 DE
 XX
 XX Human; mouse; rat; splice transcript; detection; RNA transcript;
 KW splice variant; transcriptome; oligonucleotide library; ss.
 XX
 XX Homo sapiens.
 OS
 XX
 PN WO200210449-A2.
 XX
 XX 07-FEB-2002.
 PD
 XX
 XX 20-UTL-2001; 2001WO-1B01903.
 PF
 XX
 XX 28-UTL-2000; 2000US-221607P.
 PR
 XX 02-MAY-2001; 2001US-287724P.
 XX
 XX (COMP-) COMPUGEN INC.
 PA
 XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
 PI
 XX
 XX WPI; 2002-257383/30.
 DR
 XX
 XX New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNAs transcribed from a transcription unit of
 PT a genome, useful for detecting tissue-, pathology-, and
 PT developmental-specific genes -
 PT
 XX
 PS Example 1; SEQ ID 8208; 47pp; English.
 XX
 XX The present invention describes oligonucleotide libraries for detecting
 CC messenger RNAs that populate a (sub-)transcriptome, where the
 CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple

transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridizing selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterizing the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue- and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

Sequence 60 BP; 15 A; 11 C; 18 G; 16 T; 0 other;

Query Match 1.0%; Score 22.6; DB 24; Length 60;
Best Local Similarity 64.2%; Pred. No. 4.4e+04;
Matches 34; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1030 CGTCTGGAGCTGTCTCTCGGAGCGCTGAGAGTTCAGCTATCCTTTCTT 1082
2 CGTCTGGAGCTGTGAGCCTGAGGCGAGCGATATCAAGAGCATGCAATTTT 54

RESULT 38
ABN46663/C
ID ABN46663 standard; DNA; 60 BP.

XX ABN46663;

XX 15-JUL-2002 (first entry)

XX Human spliced transcript detection oligonucleotide SEQ ID NO:19411.

XX Human; mouse; rat; splice transcript; detection; RNA transcript;
XX splice variant; transcriptome; oligonucleotide library; ss.

XX Homo sapiens.

XX WO200210449-A2.

XX 07-FEB-2002.

XX 20-JUL-2001; 2001WO-IB01903.

XX 28-JUL-2000; 2000US-221607P.

XX 02-MAY-2001; 2001US-287724P.

XX (COMP-) COMPUGEN INC.

XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX WPI; 2002-257383/30.

XX New oligonucleotide libraries comprising oligonucleotides which
XX selectively hybridize to mRNAs transcribed from a transcription unit of
XX a genome, useful for detecting tissue-, pathology-, and
XX developmental-specific genes

XX Example 1; SEQ ID 19411; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the
XX (sub-)transcriptome comprises messenger RNAs transcribed from multiple

transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridizing selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterizing the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue- and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

Sequence 60 BP; 10 A; 18 C; 14 G; 18 T; 0 other;

Query Match 1.0%; Score 22.6; DB 24; Length 60;
Best Local Similarity 64.2%; Pred. No. 4.4e+04;
Matches 34; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1534 CAAAAGCTGAGAGGAGAGTGTGAGCATCTCGTCAAGGTGAACAAGACTC 1686
DB 60 CATAAGCTGAGAGTCTCTCAATGAGGATTCGTCGCCGATTAACAAGACC 8

RESULT 39
AAQ69313
ID AAQ69313 standard; DNA; 44 BP.

XX AAQ69313;

XX 22-FEB-1995 (first entry)

XX Human sodium/potassium ATPase alpha 3 subunit gene, target region.

XX DNA protein-binding assay; test sequence; screening sequence;
XX promoter; target; TATA box; Herpes Simplex Virus; HSV;
XX origin of replication; UL9; transcription factor; TFIID;

XX ATP1 A3; ds.

XX Synthetic.

XX WO9414980-A.

XX 07-JUL-1994.

XX 20-DEC-1993; 93WO-US12388.

XX 23-DEC-1992; 92US-0996783.

XX 17-SEP-1993; 93US-0123936.

XX (GENE-) GENELABS TECHNOLOGIES INC.

XX Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;

XX WPI; 1994-234711/28.

XX Sequence-directed DNA-binding molecules - useful in
XX pharmaceuticals and as molecular reagents

XX Claim 28; Page 243; 587pp; English.

XX A DNA protein-binding assay is provided, useful for screening
XX libraries of synthetic or biological cpds. for their ability
XX to bind DNA test sequences. The assay is versatile in that any

CC number of test sequences can be tested by placing the test sequence
 CC adjacent to a defined protein-binding screening sequence. Binding
 CC of mols. to these test sequences changes the binding characteristics
 CC of the protein mol. to its cognate binding sequence. When such a mol.
 CC binds the test sequence, the equilibrium of the DNA:protein complexes
 CC is disturbed, generating changes in the concentration of free DNA probe.
 CC One application of this method is to eucaryotic general transcription
 CC factors (e.g. TFIID), where the target region is typically selected
 CC from DNA sequences adjacent to the binding site for the eucaryotic
 CC transcription factor. Numerous exemplary test sequences are given:
 CC the sequences in AA069251-731 and AA069850 correspond to promoter
 CC targets (typically, TATA box-contg. sites) for human genes and the
 CC sequences in AA069732-849 correspond to promoter targets for viral genes.
 CC The test sequences may also be randomly generated. DNA:protein
 CC interaction may be used for screening purposes, e.g. the Herpes Simplex
 CC Virus (HSV) origin of replication and UL9 (see AA069851-52, AA069865 and
 CC AA069891).

XX Sequence 44 BP; 6 A; 15 C; 20 G; 3 T; 0 other;

XX Query Match 1.0%; Score 22.4; DB 15; Length 44;

XX Best Local Similarity 72.5%; Pred. No. 4.2e+04; Mismatches 11; Indels 0; Gaps 0;

QY 9 CTGCGCGGTCGCGGCCCATGAGCGCAGAGAGCGCG 48
 Db 4 CTCGCCGCGACGCGGCGATATGAGAGCGCAGAGCGCGCG 43

RESULT 40

AA063775 AAT63775 standard; DNA; 44 BP.

XX AAT63775;

DT 13-MAR-1997 (first entry)

XX Human Na/K ATPase alpha 3 subunit (ATP1 A3) gene TFIID binding site.

XX Duplex DNA: target region; binding characteristic; DNA binding protein;

XX TFIID; transcription factor; binding site; inhibition; enhance;

XX cancer; inherited genetic disorder; ds.

XX Homo sapiens.

XX US5578444-A.

XX 26-NOV-1996.

XX 27-JUN-1991; 91US-0723618.

XX 20-DEC-1993; 93US-0171389.

XX 27-JUN-1991; 91US-0723618.

XX 23-DEC-1992; 92US-0996783.

XX 17-SEP-1993; 93US-0123936.

XX (GENE-) GENELABS TECHNOLOGIES INC.

XX Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;

XX WPI; 1997-020402/02.

XX Altering binding characteristics of DNA binding proteins to duplex

XX DNA - by attaching specific small cpd. to target region close to the

XX Protein's binding site, useful in treatment of viral disease, cancer

XX etc

PS Claim 6; Column 131; 264pp; English.

CC The sequences given in AAT63713-4312 represent duplex DNA's which act.

CC as target regions in the method of the invention. The method for

CC altering the binding characteristics of a DNA-binding protein to duplex

CC DNA comprises contacting the duplex DNA with a small molecule which

CC binds sequence-specifically to a target region, where, when the small
 CC molecule is bound to the target region, it is adjacent to, but not
 CC overlapping by more than 4 bp, a binding site for a DNA-binding protein.
 CC The small molecule is added at a concentration effective to alter the
 CC binding of the DNA binding protein, pref. TFIID, to its binding site on
 CC the duplex DNA. The binding of the small molecule may inhibit or
 CC enhance the binding of the DNA-binding protein to its binding site. The
 CC compounds isolated using this method are potentially useful as
 CC therapeutic agents for treatment of any disease which involves a
 CC specific DNA sequence, e.g. cancer, or inherited genetic disorders etc.
 CC The method is suitable for screening large biological or chemical
 CC libraries and allows determination of sequence-specific and relative
 CC affinities of known DNA-binding agents for different DNA sequences.
 CC The design of these duplex DNA's allows a single DNA:protein interaction
 CC to be used for screening sequence-specific, or preferential, DNA binding
 CC proteins that recognise almost any possible sequence (see also AAT9539-
 CC 74).

XX Sequence 44 BP; 6 A; 15 C; 20 G; 3 T; 0 other;

XX Query Match 1.0%; Score 22.4; DB 18; Length 44;

XX Best Local Similarity 72.5%; Pred. No. 4.2e+04; Mismatches 11; Indels 0; Gaps 0;

QY 9 CTGCGCGGTCGCGGCCCATGAGCGCAGAGAGCGCG 48
 Db 4 CTCGCCGCGACGCGGCGATATGAGAGCGCAGAGCGCGCG 43

RESULT 41

AA017063 AAX17063 standard; DNA; 44 BP.

XX AAX17063;

DT 06-MAY-1999 (first entry)

XX Test sequence from human sodium/potassium ATPase alpha 3 subunit.

XX Test sequence; DNA-binding molecule; screening sequence; human;

XX nucleic acid amplification; target; viral; ds.

XX Homo sapiens.

XX US5869241-A.

XX 09-FEB-1999.

XX 07-JUN-1995; 95US-0475228.

XX 20-DEC-1993; 93US-0171389.

XX 27-JUN-1991; 91US-0723618.

XX 23-DEC-1992; 92US-0996783.

XX 17-SEP-1993; 93US-0123936.

XX 07-JUN-1995; 95US-0475228.

XX (GENE-) GENELABS TECHNOLOGIES INC.

XX Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;

XX WPI; 1999-152755/13.

XX Determination of DNA sequence preference of a DNA-binding molecule -

XX based on inhibition of binding of protein to oligonucleotide

XX sequence attached to test sequence

XX Claim 3; Columns 131-132; 270pp; English.

CC Sequences AAX17001 to AAX17600 represent specifically claimed target

CC test sequences that are used in the method of the invention of

CC determining the DNA sequence preference of a DNA-binding molecule. The

CC method comprises: (1) adding a test molecule and a DNA-binding protein to

CC a mixture of duplex DNA test oligonucleotides, each of the test

CC oligonucleotides having a test sequence adjacent to a screening sequence,
 CC where the screening sequence binds to the DNA-binding protein with a
 CC binding affinity that is independent of the DNA sequence of the test
 CC sequence, and where the mixture of duplex DNA test oligonucleotides
 CC includes several test sequences; (ii) incubating the test molecule, the
 CC mixture of duplex DNA test oligonucleotides and the DNA-binding protein
 CC for a time sufficient to permit binding of the test molecule to test
 CC sequences in the duplex DNA; (iii) separating unbound test
 CC oligonucleotides from test oligonucleotides bound to binding protein;
 CC (iv) amplifying the unbound test oligonucleotides; (v) repeating steps
 CC (ii) to (iv); (vi) isolating the amplified test oligonucleotides; and
 CC (vii) sequencing the isolated test oligonucleotides. Test sequences
 CC AAX17001-X17481 and AAX17600 correspond to promoter targets for human
 CC genes and test sequences AAX17482-X17599 correspond to promoter targets
 CC for viral genes.

CC Sequence 44 BP; 6 A; 15 C; 20 G; 3 T; 0 other;

Query Match 1.0%; Score 22.4; DB 20; Length 44;

Best Local Similarity 72.5%; Pred. No. 4.2e+04; Mismatches 11; Indels 0; Gaps 0;

Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 9 CTGCGCGGCGTCCGCCCATGAGCGACGAGAGCGCG 48
 4 CTCCCGCGAGCGCGCATATGAGAGCGGAGCGCGCG 43

RESULT 42

ABK82554
 ID ABK82554 standard; DNA; 44 BP.

AC ABK82554;

DT 27-AUG-2002 (first entry)

DE DNA binding molecule screening method test sequence #63.

XX DNA binding molecule screening; inhibition of transcription;

KW infection; human immunodeficiency virus; HIV; parasite; cancer;

KW cardiovascular; respiratory; gastrointestinal; endocrine; metabolic;

KW rheumatic; immunological; haematological; neurological;

KW psychiatric; dermatological; ophthalmological; musculo-skeletal;

XX urogenital disorder; ss.

XX Synthetic.

PN US6384208-B1.

PD 07-MAY-2002.

PF 15-JUL-1999; 99US-0354947.

XX 20-DEC-1993; 93US-0171389.

PR 07-JUN-1995; 95US-0482080.

PR 27-JUN-1991; 91US-0723618.

PR 23-DEC-1992; 92US-0996783.

PR 17-SEP-1993; 93US-0123936.

XX (GENE-) GENELABS TECHNOLOGIES INC.

PI Edwards CA, Cantor CR, Andrews BM, Turin LM, Fry KE;

DR WPI; 2002-442819/47.

XX Decreasing transcriptional activity of genes for treating infections or
 PT cancer, by administration of an agent that binds to two non-overlapping
 PT regions of the gene -
 XX Example 15; SEQ ID No 63; 98pp; English.
 XX The invention relates to a method of decreasing transcriptional activity
 CC in a duplex deoxyribonucleic acid (DNA) template (T1) comprising
 CC contacting (T1) with a binding agent comprising at least one small duplex

CC DNA-binding molecule (T2) coupled to at least one other small duplex-
 CC binding molecule that binds to a non-overlapping region of target
 CC sequence (T3). The method is useful for inhibiting transcription of a
 CC range of disease-related genes for treating infections (by viruses,
 CC including human immunodeficiency virus, bacteria, fungi, protozoa
 CC and parasites), cancer, cardiovascular, respiratory, gastrointestinal,
 CC endocrine/metabolic, rheumatic/immunological, haematological,
 CC neurologic, psychiatric, dermatological, ophthalmological,
 CC musculo-skeletal, genetic or urogenital disorders. The method provides
 CC sequence-specific inhibition of transcription of pathological genes
 CC without affecting transcription of cellular genes regulated by the same
 CC transcription factor, and can be applied to regulation of any gene.
 CC ABK82492-ABK83155 represent DNA binding molecule test sequences used in
 CC the method of the invention.

CC Sequence 44 BP; 6 A; 15 C; 20 G; 3 T; 0 other;

Query Match 1.0%; Score 22.4; DB 24; Length 44;

Best Local Similarity 72.5%; Pred. No. 4.2e+04; Mismatches 11; Indels 0; Gaps 0;

Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 9 CTGCGCGGCGTCCGCCCATGAGCGACGAGAGCGCG 48
 4 CTCCCGCGAGCGCGCATATGAGAGCGGAGCGCGCG 43

RESULT 43

AAF29313/c
 ID AAF29313 standard; DNA; 48 BP.

AC AAF29313;

DT 18-APR-2001 (first entry)

DE Primer base sequence used to illustrate primer selection method.

XX Primer; optimum sequence; differential display; ss.

OS Synthetic.

PN JP2000308487-A.

PD 07-NOV-2000.

PF 30-MAR-1999; 99JP-0088410.

PR 30-MAR-1999; 99JP-0088410.

PA (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.

DR WPI; 2001-046077/06.

XX Selection of primer base for optimizing primer selection comprises

PT obtaining an optimum sequence for differential display from an

PT expression gene data base -

XX Disclosure; Fig 9; 13pp; Japanese.

XX This invention relates to a method for selecting the sequence of a

CC primer. The method comprises obtaining an optimum sequence for

CC differential display from an expression gene data base, and using the

CC base sequences most frequently expressed as the primer candidates in the

CC order of frequency. The optimum primer group characterised by the use of

CC genetic algorithm from the primer candidates is selected. The method is

CC used for selecting a primer sequence quickly. The present sequence

CC represents a primer used in an illustration of the method of the

CC invention.
 CC Sequence 48 BP; 15 A; 3 C; 3 G; 27 T; 0 other;
 Query Match 1.0%; Score 22.4; DB 22; Length 48;
 Best Local Similarity 66.7%; Pred. No. 4.4e+04;
 Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

KW nervous system disease; ss.
 XX Homo sapiens.
 XX WO200147944-A2.
 XX 05-JUL-2001.
 PD 28-DEC-2000; 2000WO-US95498.
 PF 28-DEC-1999; 99US-0173419.
 PR 27-DEC-2000; 2000US-0173419.
 XX (CURA-) CURAGEN CORP.
 PA Shinkets RA, Leach M;
 PI WPI; 2001-465210/50.
 DR Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 XX oncoproteins and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -
 PS Claim 1; Page 2912; 4143pp; English.
 XX The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncoproteins,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukin,
 CC G-protein coupled receptors and thioesterases. The present sequence is
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded
 CC by them may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.
 CC Sequence 51 BP; 18 A; 6 C; 5 G; 22 T; 0 other;
 SQ
 Query Match 1.0%; Score 22.4; DB 22; Length 51;
 Best Local Similarity 66.7%; Pred. No. 4.6e+04;
 Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
 QY 1592 GTATGAATCTATGACAGCAATGCTTTTAATGAATTTAAGCAAAA 1639
 Db 4 GTAGATTTTATTAACAGCAATTTTCTATCAATTCAGATCTTAA 51
 XX
 RESULT 47
 AA069462
 ID AA069462 standard; DNA; 45 BP.
 XX
 AC AA069462;
 XX
 DT 27-FEB-1995 (first entry)
 XX
 DE Human interleukin 4 gene, target region.
 XX
 KW DNA protein-binding assay; test sequence: screening sequence;
 KW promoter; target; TATA box; Herpes Simplex Virus; HSV;
 KW origin of replication; UL9; transcription factor; TFIID; ds.
 XX
 OS Synthetic.
 XX
 PN WO9414980-A.
 XX
 PD 07-JUL-1994.
 XX

PF 20-DEC-1993; 93WO-US12388.
 XX 23-DEC-1992; 92US-0996783.
 PR 17-SEP-1993; 93US-0123936.
 XX
 PA (GENE-) GENELABS TECHNOLOGIES INC.
 XX
 PI Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;
 DR WPI; 1994-234711/28.
 XX
 PT Sequence-directed DNA-binding molecules - useful in
 PT pharmaceuticals and as molecular reagents
 PS Claim 28; Page 318; 587pp; English.
 XX
 CC A DNA protein-binding assay is provided, useful for screening
 CC libraries of synthetic or biological cpds. for their ability
 CC to bind DNA test sequences. The assay is versatile in that any
 CC number of test sequences can be tested by placing the test sequence
 CC adjacent to a defined protein-binding, screening sequence. Binding
 CC of mols. to these test sequences changes the binding characteristics
 CC of the protein mol. to its cognate binding sequence. When such a mol.
 CC binds the test sequence, the equilibrium of the DNA:protein complex
 CC is disturbed, generating changes in the concentration of free DNA probe.
 CC One application of this method is to eucaryotic general transcription
 CC factors (e.g. TFIID), where the target region is typically selected
 CC from DNA sequences adjacent to the binding site for the eucaryotic
 CC transcription factor. Numerous exemplary test sequences are given:
 CC the sequences in AA069251-731 and AA069850 correspond to promoter
 CC targets (typically, TATA box-contg. sites) for human genes and the
 CC sequences in AA069732-849 correspond to promoter targets for viral genes.
 CC The test sequences may also be randomly generated. DNA:protein
 CC interaction may be used for screening purposes, e.g. the Herpes Simplex
 CC Virus (HSV) origin of replication and UL9 (see AA069851-52, AA069865 and
 CC AA069891).
 XX
 SQ Sequence 45 BP; 13 A; 10 C; 7 G; 15 T; 0 other;
 Query Match 0.9%; Score 22.2; DB 15; Length 45;
 Best Local Similarity 77.1%; Pred. No. 4.8e+04;
 Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 933 TGACCAAAATCCTCAATGTAACTCAATTTGCTC 967
 Db 9 TAAAGAAATTTCCAAATGTAACATTCATTCCTC 43
 XX
 RESULT 48
 AAT63924
 ID AAT63924 standard; DNA; 45 BP.
 XX
 AC AAT63924;
 XX
 DT 17-MAR-1997 (first entry)
 XX
 DE Human interleukin-4 gene TFIID binding site.
 XX
 KW Duplex DNA; target region; binding characteristic; DNA binding protein;
 KW TFIID; transcription factor; binding site; inhibition; enhance; IL-2;
 KW cancer; inherited genetic disorder; alpha-D-galactosidase A; ds.
 XX
 OS Homo sapiens.
 XX
 PN US5578444-A.
 XX
 PD 26-NOV-1996.
 XX
 PF 27-JUN-1991; 91US-0723618.
 XX
 PR 20-DEC-1993; 93US-0171389.
 PR 27-JUN-1991; 91US-0723618.
 PR 23-DEC-1992; 92US-0996783.

PR 17-SEP-1993; 93US-0123936.
 XX (GENE-) GENELABS TECHNOLOGIES INC.
 XX
 XX Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;
 PI WPI, 1997-020402/02.
 DR
 XX
 PT Altering binding characteristics of DNA binding proteins to duplex
 PT DNA - by attaching specific small cpd. to target region close to the
 PT protein's binding site, useful in treatment of viral disease, cancer
 PT etc
 PS
 PS Claim 6; Column 207-208; 264pp; English.
 CC The sequences given in AAT63713-4312 represent duplex DNA's which act
 CC as target regions in the method of the invention. The method for
 CC altering the binding characteristics of a DNA-binding protein to duplex
 CC DNA comprises contacting the duplex DNA with a small molecule which
 CC binds sequence-specifically to a target region, where, when the small
 CC molecule is bound to the target region, it is adjacent to, but not
 CC overlapping by more than 4 bp, a binding site for a DNA-binding protein.
 CC The small molecule is added at a concentration effective to alter the
 CC binding of the DNA binding protein, pref. TFIID, to its binding site on
 CC the duplex DNA. The binding of the small molecule may inhibit or
 CC enhance the binding of the DNA-binding protein to its binding site. The
 CC compounds isolated using this method are potentially useful as
 CC therapeutic agents for treatment of any disease which involves a
 CC specific DNA sequence, e.g. cancer, or inherited genetic disorders etc.
 CC The method is suitable for screening large biological or chemical
 CC libraries and allows determination of sequence-specific and relative
 CC affinities of known DNA-binding agents for different DNA sequences.
 CC The design of these duplex DNA's allows a single DNA:protein interaction
 CC to be used for screening sequence-specific, or preferential, DNA binding
 CC proteins that recognise almost any possible sequence (see also AAT49539-
 CC 74).
 CC
 SQ Sequence 45 BP; 13 A; 10 C; 7 G; 15 T; 0 other;
 XX
 XX
 Query Match 0.9%; Score 22.2; DB 18; Length 45;
 Best Local Similarity 77.1%; Pred. No. 4.8e+04;
 Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 933 TGACAAATTCCTCAATGTAACTCAATTGCTC 967
 DB 9 TAACGAAATTTCCATGTAACTCAATTGCTC 43
 RESULT 49
 AAX17212
 ID AAX17212 standard; DNA; 45 BP.
 XX
 AC AAX17212;
 XX
 DT 06-MAY-1999 (first entry)
 XX
 DE Test sequence from human interleukin 4 gene.
 KW Test sequence; DNA-binding molecule; screening sequence; human;
 KW nucleic acid amplification; target; viral; ds.
 XX
 OS Homo sapiens.
 XX
 PN US5869241-A.
 XX
 PD 09-FEB-1999.
 XX
 PF 07-JUN-1995; 95US-0475228.
 XX
 PR 20-DEC-1993; 93US-0171389.
 PR 27-JUN-1991; 91US-0723618.
 PR 23-DEC-1992; 92US-0996783.
 PR 17-SEP-1993; 93US-0123936.

PR 07-JUN-1995; 95US-0475228.
 XX (GENE-) GENELABS TECHNOLOGIES INC.
 XX
 XX Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;
 PI WPI, 1999-152755/13.
 DR
 XX
 PT Determination of DNA sequence preference of a DNA-binding molecule -
 PT based on inhibition of binding of protein to oligonucleotide
 PT sequence attached to test sequence
 PS
 PS Claim 3; Columns 209-210; 270pp; English.
 CC Sequences AAX17001 to AAX17600 represent specifically claimed target
 CC test sequences that are used in the method of the invention of
 CC determining the DNA sequence preference of a DNA-binding molecule. The
 CC method comprises: (i) adding a test molecule and a DNA-binding protein to
 CC a mixture of duplex DNA test oligonucleotides, each of the test
 CC oligonucleotides having a test sequence adjacent to a screening sequence,
 CC where the screening sequence binds to the DNA-binding protein with a
 CC binding affinity that is independent of the DNA sequence of the test
 CC sequence, and where the mixture of duplex DNA test oligonucleotides
 CC includes several test sequences; (ii) incubating the test molecule, the
 CC mixture of duplex DNA test oligonucleotides and the DNA-binding protein
 CC for a time sufficient to permit binding of the test molecule to test
 CC sequences in the duplex DNA; (iii) separating unbound test
 CC oligonucleotides from test oligonucleotides bound to binding protein;
 CC (iv) amplifying the unbound test oligonucleotides; (v) repeating steps
 CC (ii) to (iv); (vi) isolating the amplified test oligonucleotides; and
 CC (vii) sequencing the isolated test oligonucleotides. Test sequences
 CC AAX17001-X17481 and AAX17600 correspond to promoter targets for human
 CC genes and test sequences AAX17482-X17599 correspond to promoter targets
 CC for viral genes.
 CC
 SQ Sequence 45 BP; 13 A; 10 C; 7 G; 15 T; 0 other;
 XX
 XX
 Query Match 0.9%; Score 22.2; DB 20; Length 45;
 Best Local Similarity 77.1%; Pred. No. 4.8e+04;
 Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 933 TGACAAATTCCTCAATGTAACTCAATTGCTC 967
 DB 9 TAACGAAATTTCCATGTAACTCAATTGCTC 43
 RESULT 50
 ABR82703
 ID ABR82703 standard; DNA; 45 BP.
 XX
 AC ABR82703;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE DNA binding molecule screening method test sequence #212.
 KW DNA binding molecule screening; inhibition of transcription;
 KW infection; human immunodeficiency virus; HIV; parasite; cancer;
 KW cardiovascular; respiratory; gastrointestinal; endocrine; metabolic;
 KW rheumatic; immunological; haematological; neurological;
 KW psychiatric; dermatological; ophthalmological; musculo-skeletal;
 KW urogenital disorder; ss.
 XX
 OS Synthetic.
 XX
 PN US6384208-B1.
 XX
 PD 07-MAY-2002.
 XX
 PF 15-JUL-1999; 99US-0354947.
 XX
 PR 20-DEC-1993; 93US-0171389.
 PR 07-JUN-1995; 95US-0482080.

PR 27-JUN-1991; 91US-0723618.
 PR 23-DEC-1992; 92US-0996783.
 PR 17-SEP-1993; 93US-0123936.
 XX
 PA (GENE-) GENELABS TECHNOLOGIES INC.
 XX
 PI Edwards CA, Cantor CR, Andrews BM, Turin LM, Fry KE;
 DR WPI; 2002-442819/47.
 XX
 PT Decreasing transcriptional activity of genes for treating infections or
 PT cancer, by administration of an agent that binds to two non-overlapping
 CC regions of the gene
 CC
 PS Example 15; SEQ ID No 212; 98pp; English.
 XX
 CC The invention relates to a method of decreasing transcriptional activity
 CC in a duplex deoxyribonucleic acid (DNA) template (T1) comprising
 CC contacting (T1) with a binding agent comprising at least one small duplex
 CC DNA-binding molecule (T2) coupled to at least one other small duplex-
 CC binding molecule that binds to a non-overlapping region of target
 CC sequence (TS). The method is useful for inhibiting transcription of a
 CC range of disease-related genes for treating infections (by viruses,
 CC including human immunodeficiency virus, bacteria, fungi, protozoa
 CC and parasites), cancer, cardiovascular, respiratory, gastrointestinal,
 CC endocrine/metabolic, rheumatic/immunological, ophthalmological,
 CC neurological, psychiatric, dermatological, haematological,
 CC musculo-skeletal, genetic or urogenital disorders. The method provides
 CC sequence-specific inhibition of transcription of pathological genes
 CC without affecting transcription of cellular genes regulated by the same
 CC transcription factor, and can be applied to regulation of any gene.
 CC ABK82492-ABK8315 represent DNA binding molecule test sequences used in
 CC the method of the invention.
 XX

SO Sequence 45 BP; 13 A; 10 C; 7 G; 15 T; 0 other;

Query Match 0.9%; Score 22.2; DB 24; Length 45;

Best Local Similarity 77.1%; Pred. No. 4.8e+04;
 Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 933 TGACAAAATCTCAATGTAACTCAATTTGGCTC 967

DB 9 TACGAAAATTTCCAAATGTAACTCAATTTCCCTC 43

RESULT 51

AAAF29294 standard; DNA; 48 BP.

XX
 AC AAFA29294;

DT 18-APR-2001 (first entry)

XX
 DE Primer base sequence used to illustrate primer selection method.

XX
 KM Primer; optimum sequence; differential display; ss.

XX
 OS Synthetic.

XX
 PN JP2000308487-A.

PD 07-NOV-2000.

PF 30-MAR-1999; 99JP-0088410.

PR 30-MAR-1999; 99JP-0088410.

PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX
 DR WPI; 2001-046077/06.

PT Selection of primer base for optimizing primer selection comprises
 PT obtaining an optimum sequence for differential display from an

PT expression gene data base -
 XX
 PS Disclosure; Fig 9; 13pp; Japanese.
 XX

CC This invention relates to a method for selecting the sequence of a
 CC primer. The method comprises obtaining an optimum sequence for
 CC differential display from an expression gene data base, and using the
 CC base sequences most frequently expressed as the primer candidates in the
 CC order of frequency. The optimum primer group characterised by the use of
 CC genetic algorithm from the primer candidates is selected. The method is
 CC used for selecting a primer sequence quickly. The present sequence
 CC represents a primer used in an illustration of the method of the
 CC invention.
 XX

SO Sequence 48 BP; 17 A; 3 C; 2 G; 26 T; 0 other;

Query Match 0.9%; Score 22.2; DB 22; Length 48;

Best Local Similarity 69.8%; Pred. No. 5e+04;
 Matches 30; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 2097 AACAACTGAATCTTTTAAATATAATATTTTCAAA 2139

DB 5 ATCTTCTGAAGAATTTTATATATAAATTTATTTTCA 47

RESULT 52

AAAL32145 standard; DNA; 51 BP.

XX
 AC AAL32145;

DT 24-JAN-2002 (first entry)

XX
 DE Human SNP oligonucleotide #5353.

XX
 KM Immunosuppressive; immunostimulatory; antiinflammatory; cyrostatic;
 KM neuroprotective; antineutrophil; gene therapy; vaccine; amylose; cancer;
 KM amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KM cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KM complement related protein; cytochrome; kinesin; cytokine; interferon;
 KM interleukin; G-protein coupled receptor; cholesterae; inflammation;
 KM multifactorial disease; autoimmune disease; infection;
 KM nervous system disease; ss.

XX
 OS Homo sapiens.

XX
 PN WO200147944-A2.

PD 05-JUL-2001.

PF 28-DEC-2000; 2000MO-US35498.

PR 28-DEC-1999; 99US-0173419.

XX
 DR 27-DEC-2000; 2000US-0173419.

PA (CURA-) CURAGEN CORP.

XX
 PI Shimketa RA, Leach M;

XX
 DR WPI; 2001-465210/50.

PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.

XX
 PS Claim 1; Page 2927; 4143pp; English.

XX
 CC The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukin,
 CC G-protein coupled receptors and thioesterases. The present sequence is

CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukemia), diseases of the nervous system and an infection of pathogenic
CC organisms.

SO Sequence 51 BP; 15 A; 7 C; 2 G; 27 T; 0 other;

Query Match 0.9%; Score 22.2; DB 22; Length 51;
Best Local Similarity 69.8%; Pred. No. 5.1e+04;
Matches 30; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 2110 TTTTATTAATATATTTTTCATATTTTCAATATTTTCAATTTTTCATT 2152
Db 2 TTTCTTTATATATACATATTTTCTCAATACATATGTTATT 44

RESULT 53

ABN40059
ID ABN40059 standard; DNA; 60 BP.

AC ABN40059;

XX 15-JUL-2002 (first entry)

DE Human spliced transcript detection oligonucleotide SEQ ID NO:12807.

XX Human; mouse; rat; splice transcript; detection; RNA transcript;

KM splice variant; transcriptome; oligonucleotide library; ss.

XX Homo sapiens.

XX WO200210449-A2.

XX 07-FEB-2002.

XX 20-JUL-2001; 2001MO-IB01903.

XX 28-JUL-2000; 2000US-221607P.

XX 02-MAY-2001; 2001US-287724P.

XX (COMP-) COMPUGEN INC.

XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX WPI; 2002-257383/30.

XX New oligonucleotide libraries comprising oligonucleotides which

XX selectively hybridize to mRNAs transcribed from a transcription unit of

XX a genome, useful for detecting tissue-, pathology-, and

XX developmental-specific genes

XX Example 1; SEQ ID 12807; 47bp; English.

XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the
XX (sub-)transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises
XX several oligonucleotides, each capable of hybridizing selectively to a
XX set of messenger RNAs transcribed from a given transcription unit of
XX the genome, which encodes one or more messenger RNA splice variants.
XX The oligonucleotide libraries are useful for detecting mRNAs from a
XX biological sample, in expression profiling studies, in qualitatively or
XX quantitatively characterizing the corresponding transcriptome, and in
XX detecting RNA transcripts and splice variants of human or animal
XX transcriptomes. The libraries may also be used as specialised mini
XX libraries to detect transcripts of a sub-transcriptome under a
XX particular biological or pathological state, and so allowing the

CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN55589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.int/pub/published_pct_sequences.

SO Sequence 60 BP; 16 A; 10 C; 21 G; 13 T; 0 other;

Query Match 0.9%; Score 22.2; DB 24; Length 60;
Best Local Similarity 61.0%; Pred. No. 5.6e+04;
Matches 36; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 800 AATGATGCGCCCTGAAATGATGAGAGGCGCAATCGCTGCGATGCTGG 858
Db 2 ATTACATAGCTCCCGAGTGCTGAGCAAGAAAGGCACAGTTTCGAGTGATGTGG 60

RESULT 54

ABN5158/C
ID ABN5158 standard; DNA; 60 BP.

XX ABN5158;

XX 15-JUL-2002 (first entry)

DE Human spliced transcript detection oligonucleotide SEQ ID NO:17906.

XX Human; mouse; rat; splice transcript; detection; RNA transcript;

KM splice variant; transcriptome; oligonucleotide library; ss.

XX Homo sapiens.

XX WO200210449-A2.

XX 07-FEB-2002.

XX 20-JUL-2001; 2001MO-IB01903.

XX 28-JUL-2000; 2000US-221607P.

XX 02-MAY-2001; 2001US-287724P.

XX (COMP-) COMPUGEN INC.

XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX WPI; 2002-257383/30.

XX New oligonucleotide libraries comprising oligonucleotides which

XX selectively hybridize to mRNAs transcribed from a transcription unit of

XX a genome, useful for detecting tissue-, pathology-, and

XX developmental-specific genes

XX Example 1; SEQ ID 17906; 47bp; English.

XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the
XX (sub-)transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises
XX several oligonucleotides, each capable of hybridizing selectively to a
XX set of messenger RNAs transcribed from a given transcription unit of
XX the genome, which encodes one or more messenger RNA splice variants.
XX The oligonucleotide libraries are useful for detecting mRNAs from a
XX biological sample, in expression profiling studies, in qualitatively or
XX quantitatively characterizing the corresponding transcriptome, and in
XX detecting RNA transcripts and splice variants of human or animal
XX transcriptomes. The libraries may also be used as specialised mini
XX libraries to detect transcripts of a sub-transcriptome under a
XX particular biological or pathological state, and so allowing the

CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27553 to ABN5589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at [ftp.wipo.int/pub/published_pat_sequences](http://wipo.int/pub/published_pat_sequences).

Sequence 60 BP; 9 A; 26 C; 1 G; 24 T; 0 other;

Query Match	0.98; Score 22.2; DB 24; Length 60;
-------------	-------------------------------------

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Matches    36;  Conservative    0;  Mismatches    23;  Indels    0;  Gaps    0;

```

Qy 309 TCGGCTACTTGTTAAAGGGGCTATGAAAGTTCCTCAAGTCGAAAAGTAAACGAG 367
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 60 TAGGCTAATTAGGAATGGGGTAATGCAGAGTGAGAAAAGCAAGAGAATTAAGTAG 2

RESULT 55	
AAH44211/c	
ID	AAH44211 standard; DNA; 33 BP.

AC AAH44211;

DT 20-SEP-2001 (first entry)

DE p70 S6K mutagenesis PCR primer #2.

KW Protein kinase; identification; hydrophobic pocket; interacting;
KW cancer; diabetes; inhibition; apoptosis; tissue injury;
KW ischaemic injury; stroke; PCR primer; mutagenesis; ss.

OS	Homo sapiens.
OS	Synthetic.

PN WO200144497-A2

21-JUN-2001.

PF 04-DEC-2000; 2000WO-GB04598.

PR 02-DEC-1999; 99US-0168559.

PA (UYDU-) UNIV DUNDEE

PI Alessi D, Biondi R;

DR WPI; 2001-390252/41.

PT Identifying modulators of protein kinase (PK) activity, useful in
PT developing drugs for treating cancer or diabetes, by measuring the
PT ability of the compound to modulate or mimic the interaction of PK with
PT interacting polypeptides -

PS Example 1; Page 72; 180pp; English.

The present invention describes a method for identifying a compound that modulates protein kinase activity. The method comprises measuring the ability of the compound to inhibit, promote or mimic the interaction of a hydrophobic pocket-containing protein kinase with an interacting polypeptide. The interacting polypeptide interacts with the hydrophobic pocket of the protein kinase and/or comprises the amino acid sequence Phe/Tyr-Xaa-Xaa-Phe/Tyr (I). The method is useful in screening assays for identifying pharmaceutical compounds or drugs. Compounds, polypeptides or polynucleotides from the present invention are useful in medicine, particularly in the manufacture of a medicament for treating a patient in need of modulation of signalling by a hydrophobic pocket-containing protein kinase. Specifically, the patient has cancer or diabetes or is in need of inhibition of apoptosis, e.g. a patient suffering from tissue

injury or ischemic injury, including stroke. The compound or composition is also useful for inhibiting the degree or rate of phosphorylation by the protein kinase. The interacting polypeptide or compound is useful in methods of stabilizing a hydrophobic pocket-containing protein kinase, where the protein kinase is exposed to the compound or polypeptide. AAB99786 to AAB99847 represent amino acid sequences, and A4444210 and A4444211 represent oligonucleotide sequences, used in the exemplification of the present invention.

Sequence 33 BP; 8 A; 10 C; 9 G; 6 T; 0 other;

Query Match	Score	DB	Length
0.9%	22	22	33

Matches	22;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
---------	-----	--------------	----	------------	----	--------	----	------	----

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QY      1269  GGCTCCATCTGTACTTGAAGT  1290
          |||||
Db      33    GGCTCCATCTGTACTTGAAGT  12

```

RESULT 56
ABA96305/c
ID ABA96305 standard; DNA; 39 BP.

AC ABA96305;

DT 18-MAR-2002 (first entry)

LDL receptor allele-specific probe GC15 B.

AA Amplification product; pharmacogenetic testing; forensic; virus; SNP
 KW anthropology; paternity testing; pathogen; bacteria; yeast; HIV;
 KW single nucleotide polymorphism; mini-sequencing; mutation;
 KW triplet repeat expansion; chromosome rearrangement; cystic fibrosis;
 KW sickle-cell anaemia; LDL receptor; probe; ss.

OS Synthetic.

PN WO200183823-A1

PD 08-NOV-2001.

PF 30-APR-2001; 2001WO-US13979.

PR 28-APR-2000; 2000US-200635P.

PA (QUAN-) QUANTUM. DOT CORP.

PI Lai JH, Phillips VE, Watson AR;

DR WPI; 2002-114152/15.

PT Analysis of polynucleotides in a sample using generic capture sequences
PT comprises amplifying target polynucleotide, and utilizing the product
PT to indirectly assay the sample for the polynucleotide -

PS Example 2; Page 47; 85pp; English.

CC The invention relates to assaying for an amplification product from a
CC target polymucleotide. An amplification reaction is used to produce the
CC amplification product from the target polymucleotide so that it can be
CC used to indirectly assay the sample for the target polymucleotide. A
CC sample suspected of containing the target polymucleotide is contacted
CC with first and second primers to amplify the target polymucleotide; the
CC first primer comprises a tag sequence, the complement of which is formed
CC on the opposite strand during amplification and is referred to as a
CC capture label. A capture probe is provided that is conjugated to a
CC substrate and can bind to the capture sequence to form an amplification
CC product detection complex. Identification of the label in association
CC with the substrate demonstrates that the amplification product was formed
CC the target polymucleotide was present in the sample. The method is useful
CC for pharmacogenetic testing, for forensic or anthropological setting to
CC identify a species or individual which was the source of a specimen.

CC The method can also be used for paternity testing, testing for
 CC compatibility of prospective tissue or blood donors and in screening for
 CC hereditary disorders. Other applications include gene expression studies,
 CC human population genetics, to detect contaminants or pathogens including
 CC bacteria, yeast, viruses, for HIV subtyping and to detect single
 CC nucleotide polymorphisms associated with particular alleles or subsets of
 CC alleles. The method is also useful for mini-sequencing and for detection
 CC of mutations, including without limitation SNPs, insertions, deletions,
 CC transversions, frame shifts, triplet repeat
 CC expansions and chromosome rearrangements. The method is useful to detect
 CC nucleotide sequences associated with increased risk of diseases or
 CC disorders, including cystic fibrosis, Tay-Sachs and sickle-cell anaemia.
 CC The present sequence is that of a probe for detection of allele-specific
 CC genomic DNA sequences from the LDL receptor in the method of the
 CC invention.

SO Sequence 39 BP; 3 A; 5 C; 5 G; 26 T; 0 other;
 Query Match 0.9%; Score 22; DB 24; Length 39;
 Best Local Similarity 73.7%; Pred. No. 5.1e+04;
 Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1763 AATCATCATGTGCGAATAAATACTTAAGCAAA 1800
 Db 39 AATCAGTCACTGCGCCGAGAAAAAATAAATAA 2

RESULT 57
 AAX76470
 ID AAX76470 standard; DNA; 42 BP.
 AC AAX76470;
 XX
 DT 05-AUG-1999 (first entry)
 DE Human BRCA1 interacting protein gene B112 PCR primer B112.2J.
 XX
 KM Human; BRCA1 interacting protein; B112; CtIP; tumour suppressor;
 KM cancer; therapy; PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 PN WO9927075-A1.
 PD 03-JUN-1999.
 XX
 PF 20-NOV-1998; 98WO-US24831.
 XX
 PR 21-NOV-1997; 97US-0975703.
 XX
 PA (MYRI-) MYRIAD GENETICS INC.
 XX
 PI Bartel PL, Tavtigian SV, Teng DHF, Wong AKC;
 XX
 DR WPI; 1999-357827/30.
 XX
 PT A carboxy-terminal BRCA1 interacting protein
 XX
 PS Example 4; Page 42; 93pp; English.
 XX
 CC The present invention describes a human BRCA1 interacting protein,
 CC designated B112. BRCA1 is a tumour suppressor protein. Methods and
 CC compositions from the present invention are useful for diagnosis of,
 CC determining predisposition to, or lack of predisposition to, and
 CC treatment of human cancer, such as breast or pancreatic cancer, as a
 CC result of a mutation in CtIP or BRCA1. The methods and compositions can
 CC also be used in rational drug design for cancer therapeutics. The
 CC present sequence represents a PCR primer for B112 which is used in an
 CC example from the present invention.

SO Sequence 42 BP; 15 A; 11 C; 10 G; 6 T; 0 other;

Query Match 0.9%; Score 22; DB 20; Length 42;
 Best Local Similarity 73.7%; Pred. No. 5.3e+04;
 Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2034 TTTTCCAGCGCAAAATGGAAGCAAGACAAAGAA 2071
 Db 2 TTTTCCAGTCACTGCGCCGAGAAAAAATCAACAGAAACA 39

RESULT 58
 AAZ67996
 ID AAZ67996 standard; DNA; 47 BP.
 AC AAZ67996;
 XX
 DT 10-SEP-2001 (first entry)
 DE Human map-related diallelic marker SEQ ID NO:2343.
 XX
 KM Human genome; diallelic marker; high density disequilibrium map;
 KM genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KM haplotyping; hybridisation; identification; characterisation;
 KM diagnosis; single nucleotide polymorphism; SNP; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT variation /tag = a
 FT /standard_name = "single nucleotide polymorphism"
 XX
 PN WO9954500-A2.
 PD 28-OCT-1999.
 XX
 PF 21-APR-1999; 99WO-IB00822.
 XX
 PR 21-APR-1998; 98US-0082614.
 PR 23-NOV-1998; 98US-0109732.
 XX
 PA (BEST) GENSET.
 XX
 PI Cohen D, Blumenfeld M, Chumakov I;
 XX
 DR WPI; 2000-013267/01.
 XX
 PT Novel diallelic markers used to construct a high density disequilibrium
 PT map of the human genome -
 XX
 PS Claim 3; Page 730; 2745pp; English.
 XX
 CC AAZ65654 to AAZ69578 represent human diallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the diallelic markers. The diallelic markers of the
 CC invention have a variety of uses: they can be used for high density
 CC mapping of the human genome, and in complex association studies and
 CC haplotyping studies which are useful in determining the genetic basis
 CC for disease states. Compositions and methods of the invention can also
 CC be useful for the identification of the targets for the development of
 CC pharmaceutical agents and diagnostic methods, as well as the
 CC characterisation of the differential efficacious responses to and side
 CC effects from pharmaceutical agents acting on a disease as well as other
 CC treatment.
 CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
 CC and 3367, are not actually given a sequence in the sequence listing
 CC from the present invention.

SO Sequence 47 BP; 33 A; 4 C; 1 G; 9 T; 0 other;
 Query Match 0.9%; Score 22; DB 21; Length 47;
 Best Local Similarity 73.7%; Pred. No. 5.6e+04;
 Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

PR	24-NOV-1999;	99US-0167383.
XX		
XX	(CTRA-) CTRAGEN CORP.	
XX		
XX	Shinkets RA, Leach M;	
XX		
DR	WPI, 2001-355949/37.	
XX		
XX	Isolated human nucleic acids comprising one or more single nucleotide	
PT	polymorphisms, useful for treating a subject suffering from a	
PT	pathology, e.g. autoimmune diseases, ascribed to the presence of a	
PT	sequence polymorphism -	
XX		
XX	Claim 1; Page 260; 674pp; English.	
XX		
CC	AB100010 to AB101104 represent human nucleic acid oligonucleotides	
CC	comprising one or more single nucleotide polymorphisms (SNPs). AB956531	
CC	to AB956993 represent human peptides encoded by some of the SNP	
CC	oligonucleotides. The sequences from the present invention can have	
CC	immunosuppressive, cytostatic, antiinflammatory, neuroprotective and	
CC	antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides	
CC	and antibodies from the present invention can be used for treating a	
CC	subject suffering from, at risk for, or suspected of, suffering from a	
CC	pathology ascribed to the presence of a sequence polymorphism. The	
CC	pathology may be autoimmune diseases, inflammation, cancer, diseases of	
CC	the nervous system, and infection by pathogenic microorganisms. The SNPs	
CC	are also useful for determining which forms of a characterised	
CC	polymorphism are present in individuals. The antibodies may be used in	
CC	the detection, quantitation and/or cellular or tissue localisation of a	
CC	polymorphic protein (e.g., for use in measuring levels of the	
CC	polymorphic protein within appropriate physiological samples).	
XX		
SQ	Sequence 50 BP; 16 A; 4 C; 8 G; 22 T; 0 other;	
XX		
Query Match	0.9%; Score 22; DB 23; Length 50;	
Best Local Similarity	67.4%; Pred. No. 5.7e+04;	
Matches 31; Conservative	0; Mismatches 15; Indels 0; Gaps 0	
Oy	2096 A A A C A C C G A A T C T T T T T T A T A T A A T A T A T T T T C A A A T A 2141	
Db	48 A A A C A A T C T T T A C A C A C T T T G G A A A A A A T A G C A T A T T T C A A A T A 3	
RESULT 62		
ID	AAL30100/c	
AC	AAL30100 standard; DNA; 51 BP.	
XX		
AC	AAL30100;	
XX		
DT	24-JAN-2002 (first entry)	
XX		
DE	Human SNP oligonucleotide #3308.	
XX		
KW	Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;	
KW	neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;	
KW	amyloid protein; angiotensin; apoptosis related protein; cadherin;	
KW	cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;	
KW	complement related protein; cytochrome; kinase; cytokine; interferon;	
KW	interleukin; G-protein coupled receptor; thioesterase; inflammation;	
KW	multifactorial disease; autoimmune disease; infection;	
KW	nervous system disease; ss.	
XX		
OS	Homo sapiens.	
XX		
FN	WO200147944-A2.	
XX		
PD	05-JUL-2001.	
XX		
PF	28-DEC-2000; 2000MO-US35498.	
XX		
XX	28-DEC-1999; 99US-0173419.	
PR	27-DEC-2000; 2000US-0173419.	

PA	(CURA-) CURAGEN CORP.
XX	
PI	Shimkets RA, Leach M;
XX	
DR	WPI; 2001-465210/50.
XX	
PT	Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PR	oncogenes and histones, useful for diagnosing and treating, e.g.
PT	cancer, autoimmune diseases and infections -
XX	
PS	Claim 1; Page 2335; 4143pp; English.
XX	
CC	The present invention relates to oligonucleotides encoding polymorphic
CC	variants of proteins related to amylases, amyloid proteins, angiotensin,
CC	apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC	histones, kinases, colony stimulating factors, complement related
CC	proteins, cytochromes, kinases, cytokines, interferons, interleukins,
CC	G-protein coupled receptors and thioesterases. The present sequence is
CC	one such oligonucleotide. The oligonucleotides and the peptides encoded
CC	by them may be used in the prevention, diagnosis and treatment of
CC	diseases associated with inappropriate expression of the proteins listed
CC	above. Disorders that may be prevented, diagnosed and/or treated include
CC	multifactorial diseases with a genetic component, such as autoimmune
CC	diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC	systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC	(e.g. cancers of the bladder, brain, breast, colon and kidney,
CC	leukaemia), diseases of the nervous system and an infection of pathogenic
CC	organisms.
XX	
SQ	Sequence 51 BP; 10 A; 0 C; 4 G; 37 T; 0 other;
	Query Match 0.9%; Score 22; DB 22; Length 51;
	Best Local Similarity 67.4%; Pred. No. 5.8e+04;
	Matches 31; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
Oy	1757 TTTAAATAATCATTCATGCTGCACAAAAAAGTAAAGCAAAAATA 1802
Db	46 TTTAAATAATCATTCATTCCAAAAAAGTAAAGCAAAAATA 1
	T T T A A A T A A T C A T T C A T G C T G C A C A A A A A G T A A A G C A A A A A T A
	A A L J 1 0 1 8 / c
ID	AAJ31018 standard; DNA; 51 BP.
XX	
AC	AAJ31018;
DT	24-JAN-2002 (first entry)
XX	
DE	Human SNP oligonucleotide #4226.
XX	
KM	Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KM	neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KM	amyloid protein; angiotensin, apoptosis related protein; cadherin;
KM	cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KM	complement related protein; cytochrome; interleukin; interferon;
KM	interleukin; G-protein coupled receptor; thioesterase; inflammation;
KM	multifactorial disease; autoimmune disease; infection;
KM	nervous system disease; ss.
OS	
OS	Homo sapiens.
XX	
PV	WO200147944-A2.
XX	
PD	05-JUL-2001.
XX	
PF	28-DEC-2000; 2000WO-US35498.
XX	
PR	28-DEC-1999; 99US-0173419.
XX	
PR	27-DEC-2000; 2000US-0173419.
XX	
PA	(CURA-) CURAGEN CORP.
XX	

PI Shimkets RA, Leach M;
 XX WPI; 2001-465210/50.
 DR
 XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -
 PS Claim 1; Page 2600; 4143pp; English.
 XX
 CC The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytokines, colony stimulating factors, interferons, interleukins,
 CC G-protein coupled receptors and thioesterases. The present sequence is
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded
 CC by them may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukaemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.
 CC
 SQ Sequence 51 BP; 5 A; 6 C; 2 G; 38 T; 0 other;
 Query Match 0.9%; Score 22; DB 22; Length 51;
 Best Local Similarity 67.4%; Pred. No. 5.8e+04;
 Matches 31; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 QY 1743 AATTAAGCTGATTTTAAATCAATCAATGCGCAAAAAA 1788
 Db 49 AATTAAGCTGCTGGAAAAAGAAAAA 4
 RESULT 64
 AAL31438/C
 ID AAL31438 standard; DNA; 51 BP.
 XX
 AC AAL31438;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE Human SNP oligonucleotide #4646.
 XX
 XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 XX neuroprotective; antimicrobial; gene therapy; vaccine; amyloid; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytokine; interleukin; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200147944-A2.
 XX
 PD 05-JUL-2001.
 XX
 PF 28-DEC-2000; 2000WO-US35498.
 XX
 XX 28-DEC-1999; .99US-0173419.
 PR 27-DEC-2000; 2000US-0173419.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA, Leach M;
 XX WPI; 2001-465210/50.
 DR

XX
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -
 PS Claim 1; Page 2722; 4143pp; English.
 XX
 CC The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytokines, colony stimulating factors, interferons, interleukin,
 CC G-protein coupled receptors and thioesterases. The present sequence is
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded
 CC by them may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukaemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.
 CC
 SQ Sequence 51 BP; 10 A; 4 C; 2 G; 35 T; 0 other;
 Query Match 0.9%; Score 22; DB 22; Length 51;
 Best Local Similarity 67.4%; Pred. No. 5.8e+04;
 Matches 31; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 QY 1757 TTTAAAAATCAATCAATGTCGCAAAAAAATTAAGCAATA 1802
 Db 49 TTTAATTAACAAATTCAGTGAAGAAAAA 4
 RESULT 65
 AAH26598
 ID AAH26598 standard; mRNA; 51 BP.
 XX
 AC AAH26598;
 XX
 DT 12-NOV-2001 (first entry)
 XX
 DE Human GM-CSF gene 3' UTR AU-rich element.
 XX
 KW Granulocyte-macrophage colony stimulating factor; GM-CSF;
 KW human, AU-rich element; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 5..9
 FT /tag= a
 FT /note= "AUUUA motif"
 FT 9..13
 FT /tag= b
 FT /note= "AUUUA motif"
 FT 13..17
 FT /tag= c
 FT /note= "AUUUA motif"
 FT 30..34
 FT /tag= d
 FT /note= "AUUUA motif"
 FT 34..38
 FT /tag= e
 FT /note= "AUUUA motif"
 FT 38..42
 FT /tag= f
 FT /note= "AUUUA motif"
 FT 42..46
 FT /tag= g
 FT /note= "AUUUA motif"
 FT 46..50
 FT misc_feature

```
FT      /*tag= h  
PT      /note= "AUTYA motif"  
XX  
PN       WO200164921-A1.  
XX  
PD       07-SEP-2001.  
XX  
PF       28-FEB-2001; 2001WO-US06782.  
XX  
PR       29-FEB-2000; 2000US--0515369.  
PA        (UYCO ) UNIV COLUMBIA NEW YORK.  
PX  
PI     Fisher PB, Madireddi MT;  
DR          WPI; 2001-565508/63.  
XX  
XX  
PT      Melanoma differentiation associated gene-7 promoter capable of  
PT      treating cancer comprises directing transcription of heterologous  
PT      coding sequence encoding tumour suppressor polypeptide positioned  
PT      downstream, useful for treating cancer .  
XX  
PS      Disclosure; Fig 2C; 132pp; English.  
XX  
CC      The present sequence is that of an AU-rich sequence in the 3'  
CC      untranslated region (3'UTR) of human granulocyte-macrophage  
CC      colony stimulating factor mRNA. The presence of AU-rich elements  
CC      (AREs) in eukaryotic mRNAs correlates with rapid mRNA turnover  
CC      and post-translational control. The ARE consists of multiple AUTYA  
CC      motifs or sequences resembling it. A similar ARE sequence is found  
CC      in the 3' UTR of the human melanoma differentiation associated  
CC      gene-7 (mda-7) gene (see AAH26596). The invention provides  
CC      recombinant expression constructs in which the human Mda-7 promoter  
CC      (see AAH26595) is operably linked to a coding sequence encoding a  
CC      tumour suppressor protein. A pharmaceutical composition including a  
CC      the recombinant expression construct is used in a claimed method of  
CC      treating melanoma, neuroblastoma, astrocytoma, glioblastoma  
CC      multiforme, cervical cancer, breast cancer, colon cancer, prostate  
CC      cancer, osteosarcoma, chondrosarcoma or a cancer of the central  
CC      nervous system.  
XX  
SQ      Sequence 51 BP; 19 A; 0 C; 0 G; 32 U; 0 other;  
  
Query Match           0.9%; Score 22; DB 22; Length 51;  
Best Local Similarity   23.7%; Pred. No. 5.8e+04;  
Matches    9; Conservative 19; Mismatches 10; Indels    0; Gaps    0;  
QY      2115 TTATATTAAATAATATTTTCAATAGCTTTTGATT 2152  
DB      :.:|.|.:|.:.|:|||||.:.|:|:|:  
         4 UAUUUAUUAUUUAUUUAUUUAUUUAUUUAUUUU 41  
  
RESULT 66  
AAS19341/C  
ID      AAS19341 standard; DNA; 58 BP.  
XX  
XX      AAS19341;  
AC  
XX  
DT      20-MAR-2002 (first entry)  
DX  
DE      Oligonucleotide 5982 used to construct plasmid XL2725.  
XX  
KW      BS; DNA purification; triple helix; plasmid purification;  
KM      oligonucleotide 5982; XL2725.  
XX  
OS      Synthetic.  
XX  
FH      Key Location/Qualifiers  
FT      repeat_region 5..55  
FT      /*tag= a  
FT      /rpe_type= "TANDEM"  
FT      repeat_unit 5..7  
FT      /*tag= b
```

```

FT      /note= "CCT repeat type"
XX
XX      WO200192511-A2.
XX
XX      06-DEC-2001.
XX
XX      25-MAY-2001; 2001WO-US17122.
XX
XX      26-MAY-2000; 2000US-0580923.
XX
XX      (AVET ) AVENTIS PHARMA SA.
XX
XX      Crouzet J, Scherman D, Wils P, Blanche F, Cameron B;
XX
XX      WPI; 2002-097772/13.
XX
XX      Purifying double-stranded (ds) DNA from a solution containing dsDNA and
XX      other components, comprises passing the solution through a support
XX      comprising a covalently coupled oligonucleotide able to form a triple
XX      helix with the dsDNA.
XX
XX      Example 7.1; Page 20; 40pp; English.
XX
XX      This invention comprises a method of purifying double-stranded DNA from
XX      a solution containing the double-stranded DNA mixed with other
XX      components, comprising passing the solution through a support comprising
XX      a covalently coupled oligonucleotide capable of forming a triple helix
XX      with the double-stranded DNA by hybridisation with a specific sequence
XX      present in the double-stranded DNA. The method is useful for purifying
XX      double-stranded DNA contained in a solution and mixed with other
XX      components. The new method is a simple, rapid and effective method for
XX      DNA purification, and makes it possible to obtain especially high
XX      purities with high yields. The method enables DNA to be purified from
XX      complex mixtures comprising other nucleic acids, proteins, endotoxins,
XX      nucleases and the like. The supports may be readily recycled, and the
XX      DNAs obtained display improved properties to pharmaceutical safety.
XX      Further, the method entails only one step contrary to prior art.
XX      The present sequence represents an oligonucleotide 582 used to
XX      create the X1275 plasmid which was used in an example of the DNA
XX      purification method of the invention.
XX
XX      Sequence 58 BP; 2 A; 36 C; 1 G; 19 T; 0 other;
XX
XX      Query Match          0.9%; Score 22; DB 24; Length 58;
XX      Best Local Similarity 63.0%; Pred. 0.6.2e+04;
XX      Matches 34; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
XX
XX      123  GACACGACCAAGAGCGCGGCTCTGAGAGAGAGCTGAGAGGGGGGTCAAGTT 176
XX      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX      54  GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGATT 1
XX
XX      RESULT 67
XX      AAV04153
XX      AAV04153 standard; DNA; 60 BP.
XX
XX      AAV04153;
XX
XX      22-JUN-1998 (first entry)
XX
XX      Blood group antigen binding (Bab) adhesin DNA fragment.
XX
XX      Blood group antigen binding adhesin; Baba; Babb; infection;
XX      gastritis; acid peptic disease; therapy; diagnosis; vaccine;
XX      immunisation; ss.
XX
XX      Helicobacter pylori.
XX
XX      WO9747646-A1.
XX
XX      18-DEC-1997.
XX
XX      10-JUN-1997; 97WO-SB01009.

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XX 19-MAR-1997; 97SE-0001014.
PR 10-JUN-1996; 96SE-0002287.
XX (BORE/) BOREN T.
XX Arngvist A, Boren T, Hammarstrom L, Ilver D, Normark S;
PI Marstrom L;
XX WPI; 1998-052240/05.
XX Helicobacter pylori blood group antigen binding protein -
PT that binds fucosylated blood group antigen, useful to diagnose,
PT prevent and treat H. pylori infection
XX
XX Claim 11: Page 26; 53pp; English.
XX This DNA fragment comprises a 5' fragment of DNA coding for novel
CC Helicobacter pylori blood group antigen binding (Bab) adhesin
CC proteins that bind specifically to fucosylated blood group
CC antigens. Examples include the claimed babA (see AAV04154) and
CC babB (see AAV04155) genes of H. pylori strain CCUG 17875. The bab
CC adhesins (see also AAW1522 and AAW1523) and DNA can be used in the
CC diagnosis, treatment and/or prophylaxis of H. pylori induced
CC infections such as gastritis and acid peptic disease, e.g. by
CC active immunisation. The genes can also be used in the recombinant
CC production of Bab adhesin polypeptides.
XX
XX Sequence 60 BP; 19 A; 13 C; 16 G; 12 T; 0 other;
SQ
XX
XX Query Match 0.9%; Score 22; DB 19; Length 60;
XX Best Local Similarity 63.0%; Pred. No. 6.3e+04;
XX Matches 34; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
XX
XX 49 GACGCGCTTTTACCAAGCCCGACTTCGAGACAGGAGAACTGAGACATGCA 102
OY |||||
DB 7 GACGCGCTTTTACCAAGCGTAGCTATCAATCGGTGAAGCGCTCAATGTA 60
|||
XX
XX RESULT 68
XX AAH93339
XX ID AAH93339 standard; DNA; 60 BP.
XX
XX AAH93339;
XX
XX 04-OCT-2001 (first entry)
XX
XX Plasmodium falciparum MAL3PC polynucleotide SEQ ID NO 60.
XX
XX Human; antisense-therapy; gene-therapy; diagnostic; forensic;
XX Gene mapping; de.
XX
XX Plasmodium falciparum.
XX
XX WO200152616-A2.
XX
XX 26-JUL-2001.
XX
XX 22-DEC-2000; 2000WO-US35190.
XX
XX 23-DEC-1999; 99US-0471275.
XX 21-JAN-2000; 2000US-048725.
XX 25-APR-2000; 2000US-0552317.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-451890/48.
XX
XX Isolated polypeptide for treatment of diseases, diagnostics, raising
XX antibodies and research use -
XX
```

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PS Example 4; Page 122; 135pp; English.
XX
XX The invention relates to an isolated human polynucleotide (AAH93398)
CC encoding a novel polypeptide (AAG64527) useful in antisense-therapy and
CC gene-therapy, in diagnosis, forensics, gene mapping and identification
CC of mutations responsible for genetic disorders and other traits.
CC Polynucleotide sequences with potential homology were also identified
CC (AAH93283-AAH93356).
XX
XX Sequence 60 BP; 31 A; 4 C; 1 G; 24 T; 0 other;
SQ
XX
XX Query Match 0.9%; Score 22; DB 22; Length 60;
XX Best Local Similarity 67.4%; Pred. No. 6.3e+04;
XX Matches 31; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
XX
XX 2096 AAACACCTGATCTTTTATATATAATATATATATTTTCAATA 2141
OY |||||
DB 2 AAACACATATGATACATATATATATATATATATATATATAATA 47
|||
XX
XX RESULT 69
XX ID AEN38032 standard; DNA; 60 BP.
XX
XX AEN38032;
XX
XX 15-JUL-2002 (first entry)
XX
XX Human spliced transcript detection oligonucleotide SEQ ID NO:10780.
XX
XX Human; mouse; rat; splice transcript; detection; RNA transcript;
XX splice variant; transcriptome; oligonucleotide library; ss.
XX
XX Homo sapiens.
XX
XX WO200210449-A2.
XX
XX 07-FEB-2002.
XX
XX 20-JUL-2001; 2001WO-IB01903.
XX
XX 28-JUL-2000; 2000US-221607P.
XX 02-MAY-2001; 2001US-287724P.
XX
XX (COMP-) COMPUGEN INC.
XX
XX Shoshan A, Masserman A, Mintz E, Mintz L, Faigler S;
XX
XX WPI; 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
XX selectively hybridize to mRNAs transcribed from a transcription unit of
XX a genome, useful for detecting tissue-, pathology-, and
XX developmental-specific genes -
XX
XX Example 1; SEQ ID 10780; 47pp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the
XX (sub-)transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises
XX several oligonucleotides, each capable of hybridizing selectively to a
XX set of messenger RNAs transcribed from a given transcription unit of
XX the genome, which encodes one or more messenger RNA splice variants.
XX The oligonucleotide libraries are useful for detecting mRNAs from a
XX biological sample, in expression profiling studies, in qualitatively or
XX quantitatively characterizing the corresponding transcriptome, and in
XX detecting RNA transcripts and splice variants of human or animal
XX transcriptomes. The libraries may also be used as specialised mini
XX libraries to detect transcripts of a sub-transcriptome under a
XX particular biological or pathological state, and so allowing the
XX detection of tissue- and pathology-specific genes such as those genes
XX only expressed in specific tissue under a specific pathological
```


CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
SO Sequence 60 BP; 18 A; 14 C; 17 G; 11 T; 0 other;
Query Match 0.9%; Score 22; DB 24; Length 60;
Best Local Similarity 63.0%; Pred. No. 6.3e+04;
Matches 34; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
DY 2032 ACTTTCCTCCAGCAATGCGAGCAAGCAAGAACTTCTCAATTGATG 2085
DB 1 ACCTTGACAGCGACATGCGAGCAAGCAAGTCTCTGCCCAAGTATG 54
RESULT 70
AAT61581/c
ID AAT61581 standard; DNA; 50 BP.
AC AAT61581;
XX
XX 28-OCT-1997 (first entry)
DT
XX
XX VH and scFv antibody library VH back-primer VH 3.5.
DE
XX
XX Human; monoclonal antitumour antibody; peripheral blood lymphocyte;
KW cancer; tumorigenesis; anticancer vaccine; PCR;
KM polymerase chain reaction; ss.
XX
XX Synthetic.
OS
PN WO9702479-A2.
XX
XX 23-JAN-1997.
PD
XX
XX 28-JUN-1996; 96WO-IB01032.
PF
XX
XX 30-JUN-1995; 95US-0497647.
PR
XX
XX (UYVA) UNIV YALE.
PA
XX
XX Cai X, Garen A;
PI
XX
XX WPI; 1997-109061/10.
DR
XX
XX Prod. of human monoclonal anti-tumour antibodies - by screening a
PT fusion phage library produced using peripheral blood lymphocytes
PT from a cancer patient
XX
XX
XX Example 3; Page 39; 82pp; English.
PS
XX
XX A process for isolating and synthesising human monoclonal anti-tumour
CC antibodies has been produced. The process involves: (a) constructing at
CC least one fusion phage library from the peripheral blood lymphocytes
CC (PBLe) of a cancer patient; (b) screening for anti-tumour antibodies in
CC the phage library in a binding assay with cultured tumour cells of the
CC same type as the patient's tumour; (c) removing extraneous antibodies by
CC absorption against normal human cells; (d) cloning the phage selected in
CC step (b) and (c); (e) assaying the specificity of the cloned phage by
CC incubating the phage with at least two types of cultured normal cells;
CC and (f) further testing the specificity of cloned phage that do not bind
CC to either cell line of cultured normal cells in further binding assays
CC to cultured tumour cells derived from more than one other tumour that is
CC not the patient's tumour. The present sequence represents a VH back-
CC primer involved in the construction of VH and scFv libraries. The
CC antibodies produced can be used for diagnostic and therapeutic
CC applications and for isolating tumour antigens for studying
CC tumorigenesis or for use as anti-cancer vaccines. The human antibodies

CC have low immunogenicity in humans compared to murine monoclonal
CC antibodies (Mabs). Since the antibodies are isolated from fusion phage
CC libraries, their affinity and specificity for a tumour cell line can be
CC improved by genetic manipulations.
SO Sequence 50 BP; 6 A; 11 C; 20 G; 10 T; 3 other;
Query Match 0.9%; Score 21.8; DB 18; Length 50;
Best Local Similarity 67.4%; Pred. No. 6.5e+04;
Matches 29; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
DY 1501 GCATCGCACCCTTCCATATGACAGCCGAACTCTGGCCAT 1543
DB 43 SCAMCAGCTGACCTCGCCAGCGGCGGCGAACCCTGAGCAT 1
RESULT 71
AAT61565/c
ID AAT61565 standard; DNA; 50 BP.
AC AAT61565;
XX
XX 28-OCT-1997 (first entry)
DT
XX
XX scFv antibody library VH back-primer VH 3.5.
DE
XX
XX Human; monoclonal antitumour antibody; peripheral blood lymphocyte;
KW cancer; tumorigenesis; anticancer vaccine; PCR;
KM polymerase chain reaction; ss.
XX
XX Synthetic.
OS
PN WO9702479-A2.
XX
XX 23-JAN-1997.
PD
XX
XX 28-JUN-1996; 96WO-IB01032.
PF
XX
XX 30-JUN-1995; 95US-0497647.
PR
XX
XX (UYVA) UNIV YALE.
PA
XX
XX Cai X, Garen A;
PI
XX
XX WPI; 1997-109061/10.
DR
XX
XX Prod. of human monoclonal anti-tumour antibodies - by screening a
PT fusion phage library produced using peripheral blood lymphocytes
PT from a cancer patient
XX
XX
XX Example 1; Page 14; 82pp; English.
PS
XX
XX A process for isolating and synthesising human monoclonal anti-tumour
CC antibodies has been produced. The process involves: (a) constructing at
CC least one fusion phage library from the peripheral blood lymphocytes
CC (PBLe) of a cancer patient; (b) screening for anti-tumour antibodies in
CC the phage library in a binding assay with cultured tumour cells of the
CC same type as the patient's tumour; (c) removing extraneous antibodies by
CC absorption against normal human cells; (d) cloning the phage selected in
CC step (b) and (c); (e) assaying the specificity of the cloned phage by
CC incubating the phage with at least two types of cultured normal cells;
CC and (f) further testing the specificity of cloned phage that do not bind
CC to either cell line of cultured normal cells in further binding assays
CC to cultured tumour cells derived from more than one other tumour that is
CC not the patient's tumour. The present sequence represents a VH back-
CC primer involved in the construction of scFv libraries. The
CC antibodies produced can be used for diagnostic and therapeutic
CC applications and for isolating tumour antigens for studying
CC tumorigenesis or for use as anti-cancer vaccines. The human antibodies
CC have low immunogenicity in humans compared to murine monoclonal
CC antibodies (Mabs). Since the antibodies are isolated from fusion phage
CC libraries, their affinity and specificity for a tumour cell line can be
CC improved by genetic manipulations.

XX	Sequence	50 BP; 6 A; 11 C; 20 G; 10 T; 3 other;
QQ	Query Match	0.9%; Score 21.8; DB 18; Length 50;
BB	Best Local Similarity	67.4%; Pred. No. 6.5e+04;
MM	Matches	29; Conservative 1; Mismatches 13; Indels 0; Gaps 0
OY	1501	GGATCGGCACCACTTCCATPAGCAGCCGAATCTGCGCCAT 1543
DB	43	SCAMCAGCTGCACCTCGGCCACTCGCACCAACCCTGAGCCAT 1
RESULT	72	
ID	AAL28954	
AC	AAL28954 standard; DNA; 51 BP.	
DT	AAL28954;	
DE	24-JAN-2002 (first entry)	
XX	Human SNP oligonucleotide #2162.	
KW	Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;	
KW	neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;	
KW	amyloid protein; angiotensin; apoptosis related protein; cadherin;	
KW	cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;	
KW	complement related protein; cyclochrome; kinesin; cytokine; interferon;	
KW	interleukin; G-protein coupled receptor; thioesterase; inflammation;	
KW	multifactorial disease; autoimmune disease; infection;	
KW	nervous system disease; ss.	
OS	Homo sapiens.	
PN	WO200147944-A2.	
PP	05-JUL-2001.	
PP	28-DEC-2000; 2000WO-US35498.	
PR	28-DEC-1999; 99US-0173419.	
PR	27-DEC-2000; 2000US-0173419.	
PA	(CURA-) CURAGEN CORP.	
PI	Shimkets RA, Leach M;	
DR	WPI; 2001-465210/50.	
PT	Polyomorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,	
PT	oncogenes and histones, useful for diagnosing and treating, e.g.	
PT	cancer, autoimmune diseases and infections -	
PS	Claim 1; Page 2001; 4143pp; English.	
CC	The present invention relates to oligonucleotides encoding polymorphic	
CC	variants of proteins related to amylases, amyloid proteins, angiotensin,	
CC	apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,	
CC	histones, kinases, colony stimulating factors, complement related	
CC	proteins, cyclochromes, kinesin, cytokines, interferons, interleukins,	
CC	G-protein coupled receptors and cholesteraes. The present sequence is	
CC	one such oligonucleotide. The oligonucleotides and the peptides encoded	
CC	by them may be used in the prevention, diagnosis and treatment of	
CC	diseases associated with inappropriate expression of the proteins listed	
CC	above. Disorders that may be prevented, diagnosed and/or treated include	
CC	multifactorial diseases with a genetic component, such as autoimmune	
CC	diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,	
CC	systemic lupus erythematosus and Grave's disease), inflammation, cancer	
CC	(e.g. cancers of the bladder, brain, breast, colon and kidney,	
CC	leukaemia), diseases of the nervous system and an infection of pathogenic	
CC	organisms.	
SQ	Sequence	51 BP; 11 A; 2 C; 5 G; 33 T; 0 other;

	Query Match	0.9%; Score 21.8; DB 22; Length 51;
	Best Local Similarity	70.7%; Pred. No. 6.5e+04;
	Matches 29; Conservative	0; Mismatches 12; Indels 0; Gaps 0;
OY	2108 TCTTTTATATAATAATAATAATTTCACAAATAGATTTT	2148
DB	10 TTTTTTTTTTGTTTATAGAGTTTTCATAAAGTTT	50
	RESULT 73	
ID	AA176866	
XX	AA176866 standard; DNA; 51 BP.	
XX	AA176866;	
DT	09-NOV-2001 (first entry)	
DE	Human silent SNP containing nucleic acid SEQ:3807.	
KM	Human; single nucleotide polymorphism; SNP; genome; gene therapy;	
KW	protein therapy; vaccine; probe; diagnostic assay; detection;	
XX	quantitation; restorative therapy; polymorphic; da.	
OS	Homo sapiens.	
PM	WO200140521-A2.	
PD	07-JUN-2001.	
PF	30-NOV-2000; 2000WO-US32758.	
PR	30-NOV-1999; 99US-0168138.	
PR	29-NOV-2000; 2000US-0726173.	
PA	(CURA-) CURAGEN CORP.	
PI	Shimkrets RA, Leach M;	
DR	WPI; 2001-356160/37.	
PT	Polymorphic nucleic acid sequences, useful in genetic testing and	
PS	therapy -	
PS	Claim 1, Page 1216, 2653pp; English.	
XX	AA173060 to AA179867 represent isolated human polymorphic polynucleotide	
CC	sequences (I), which contain single nucleotide polymorphisms (SNPs).	
CC	AAM53114 to AAM53329 represent peptide sequences related to human polymorphic	
CC	polynucleotide sequences. The sequences can be used in gene and protein	
CC	therapy, and in vaccine production. (I) and the polypeptides encoded by	
CC	them may be used in the prevention, diagnosis and treatment of diseases	
CC	associated with inappropriate expression of polymorphic polypeptides.	
CC	For example, (I) may be used to treat disorders by rectifying mutations	
CC	or deletions in a patient's genome that affect the activity of	
CC	polypeptides by expressing inactive proteins or to supplement the	
CC	patients own production of polypeptide. Additionally, (I) and its	
CC	complementary sequences may also be used as DNA probes in diagnostic	
CC	assays to detect and quantitate the presence of similar nucleic acids	
CC	in samples, and therefore which patients may be in need of restorative	
CC	therapy. The polypeptides encoded by (I) may be used as antigens in the	
CC	production of antibodies specific for polymorphic polypeptides. The	
CC	antibodies may also be used to down regulate expression and activity.	
CC	The antibodies may also be used as diagnostic agents for detecting the	
CC	presence of polymorphic polypeptides in samples.	
SQ	Sequence 51 BP; 33 A; 9 C; 5 G; 4 T; 0 other;	
	Query Match	0.9%; Score 21.8; DB 22; Length 51;
	Best Local Similarity	70.7%; Pred. No. 6.5e+04;
	Matches 29; Conservative	0; Mismatches 12; Indels 0; Gaps 0;
OY	918 TGGAAGAAAACAATTGCAAAATCTCAATGTAACTCA	958

Db 10 TAGAAAAAAAAAAAAAAAAAAAAAACTCCTCAAGGAAAAAAAAACA 50

RESULT 74

ID AAV76001

AAV76001 standard; DNA; 55 BP.

AC AAV76001;

DT 16-MAR-1999 (first entry)

DE Staphylococcus aureus contig SEQ ID #1690.

KM Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.

OS Staphylococcus aureus.

XX EP786519-A2.

XX 30-JUL-1997.

PD 07-JAN-1997; 97EP-0100117.

PE 05-JAN-1996; 96US-0009861.

PR (HUMA-) HUMAN GENOME SCI INC.

PA Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunesch CA; Rosen CA;

XX WPI; 1997-374922/35.

DR Polynucleotide(s) and proteins derived from Staphylococcus aureus

PT stored on computer readable medium and used in the production of

PT anti-S.aureus vaccines

XX

XX

XX Claim 1; Page 2034; 3271pp; English.

XX This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the computer readable medium.

XX

XX Sequence 55 BP; 24 A; 9 C; 6 G; 16 T; 0 other;

XX

Query Match 0.9%; Score 21.8; DB 16; Length 55;

Best Local Similarity 70.7%; Pred. No. 6.8e+04;

Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0

Oy 2174 CCAACTTTAAATGCGAAATTAATTCGTTGGTGTGAAGAA 2214

Db 1 CCAACTTTAATATGAAATGCTGTGTAATTAACAAGATA 41

RESULT 75

AAFS6143/c

ID	AF56143	standard; DNA; 60 BP.
XX		
AC	AAFS6143;	
XX		
DT	17-APR-2001	(first entry)
XX		
DE	Staphylococcus aureus agr enhancer region #1.	
XX		
KM	Staphylococcus aureus; Sara; staphylococcal accessory regulator A;	
KW	agr; accessory gene regulator; antibacterial; Sara inhibitor;	
XX		
KW	virulence gene; staphylococcal infection; ds.	
OS	Staphylococcus aureus.	
XX		
FN	W0200103686-A2.	
XX		
PD	18-JAN-2001.	
XX		
PF	07-JUL-2000; 2000WO-US18525.	
XX		
PR	08-JUL-1999; 99US-0142793.	
XX		
PA	(UYAR-) UNIV ARKANSAS.	
XX		
PI	Hurlburt BK, Smeltzer MS, Rechlin TM;	
XX		
DR	WPI; 2001-112567/12.	
XX		
PT	Identifying inhibitors of staphylococcal Sara (accessory regulator)	
XX		
PT	which are useful for treating staphylococcal infections, comprises	
XX		
PT	using specific binding sites of Sara protein on an accessory gene	
XX		
PT	regulator locus -	
XX		
PS	Example; Fig 2; 79pp; English.	
XX		
CC	The present sequence is given in a specification relating to a method for	
XX		
CC	identifying inhibitors of Sara (staphylococcal accessory regulator)	
XX		
CC	function involved in the expression of Staphylococcal virulence genes.	
XX		
CC	The method comprises contacting a candidate inhibitor with a Sara	
XX		
CC	binding site of the agr (accessory gene regulator) locus in solution	
XX		
CC	and assessing the binding of the candidate inhibitor to the Sara	
XX		
CC	binding site of the agr locus. The identified inhibitors are useful for	
XX		
CC	preventing and treating staphylococcal infections.	
XX		
SQ	Sequence 60 BP; 17 A; 5 C; 4 G; 34 T; 0 other;	
XX		
Query Match	0.9%; Score 21.8; DB 22; Length 60;	
ABN35167	Similarity 61.4%; Pred. No. 7.1e+04;	
Matches 35; Conservative 0; Mismatches 22; Indels 0; Gaps 0;		
Oy	1709 AATGTCATTAACTAGAACACTTCGACGACAGGAAATAAAGTGTGATTTTAAAAA 1765	
DB	60 AATATTTAACGCTAATAAAATTTTACGTTAGTAAGTAATAAAACGACTAGTTAGAAA 4	
RESULT 76		
ABN35167		
ID	ABN35167 standard; DNA; 60 BP.	
XX		
AC	ABN35167;	
XX		
DT	15-JUL-2002 (first entry)	
XX		
DE	Human spliced transcript detection oligonucleotide SEQ ID NO:7915.	
XX		
KM	Human; mouse; rat; splice transcript; detection; RNA transcript;	
KW	splice variant; transcriptome; oligonucleotide library; ss.	
XX		
OS	Homo sapiens.	
XX		
FN	W0200210449-A2.	
XX		
PD	07-FEB-2002.	

XX 20-JUL-2001; 2001WO-IB01903.
 PF 28-JUL-2000; 2000US-221607P.
 PR 02-MAY-2001; 2001US-287724P.
 XX (COMP-) COMPUEN INC.
 PA Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
 PI WPI; 2002-257383/30.
 DR
 XX New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNAs transcribed from a transcription unit of
 PT a genome, useful for detecting tissue-, pathology-, and
 PT developmental-specific genes -
 XX
 PS Example 1; SEQ ID 7915; 47bp; English.
 XX
 CC The present invention describes oligonucleotide libraries for detecting
 CC messenger RNAs that populate a (sub-)transcriptome, where the
 CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
 CC transcription units that populate a genome. The library comprises
 CC several oligonucleotides, each capable of hybridizing selectively to a
 CC set of messenger RNAs transcribed from a given transcription unit of
 CC the genome, which encodes one or more messenger RNA splice variants.
 CC The oligonucleotide libraries are useful for detecting mRNAs from a
 CC biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterizing the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcriptomes. The libraries may also be used as specialised mini
 CC libraries to detect transcripts of a sub-transcriptome under a
 CC particular biological or pathological state, and so allowing the
 CC detection of tissue- and pathology-specific genes such as those genes
 CC only expressed in specific tissue under a specific pathological
 CC condition; to detect developmental specific genes; and to detect RNA
 CC transcripts and splice variants of a transcriptome of a patient suffering
 CC from a particular disorder. ABN27253 to ABN59589 represent
 CC oligonucleotide sequences from rats, humans and mice, which are used in
 CC the exemplification of the present invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).
 XX
 SQ Sequence 60 BP; 24 A; 10 C; 18 G; 8 T; 0 other;
 XX
 Query Match 0.9%; Score 21.8; DB 24; Length 60;
 Best Local Similarity 70.7%; Pred. No. 7.1e+04;
 Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 XX
 QY 974 TCACACAGAGCCAGAGATCTGCTTAAGCTGCTGAAA 1014
 Db 5 TACACAGAGAGCCAGAGATCTGCTTAAGCTGCTGAAA 45
 XX
 RESULT 77
 ABN43764/c
 ID ABN43764 standard; DNA; 60 BP.
 XX
 AC ABN43764;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Human spliced transcript detection oligonucleotide SEQ ID NO:16512.
 XX
 KW Human; mouse; rat; splice transcript; detection; RNA transcript;
 KW splice variant; transcriptome; oligonucleotide library; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200210449-A2.
 XX
 PD 07-FEB-2002.

XX 20-JUL-2001; 2001WO-IB01903.
 PF 28-JUL-2000; 2000US-221607P.
 PR 02-MAY-2001; 2001US-287724P.
 XX (COMP-) COMPUEN INC.
 PA Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
 PI WPI; 2002-257383/30.
 DR
 XX New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNAs transcribed from a transcription unit of
 PT a genome, useful for detecting tissue-, pathology-, and
 PT developmental-specific genes -
 XX
 PS Example 1; SEQ ID 16512; 47bp; English.
 XX
 CC The present invention describes oligonucleotide libraries for detecting
 CC messenger RNAs that populate a (sub-)transcriptome, where the
 CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
 CC transcription units that populate a genome. The library comprises
 CC several oligonucleotides, each capable of hybridizing selectively to a
 CC set of messenger RNAs transcribed from a given transcription unit of
 CC the genome, which encodes one or more messenger RNA splice variants.
 CC The oligonucleotide libraries are useful for detecting mRNAs from a
 CC biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterizing the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcriptomes. The libraries may also be used as specialised mini
 CC libraries to detect transcripts of a sub-transcriptome under a
 CC particular biological or pathological state, and so allowing the
 CC detection of tissue- and pathology-specific genes such as those genes
 CC only expressed in specific tissue under a specific pathological
 CC condition; to detect developmental specific genes; and to detect RNA
 CC transcripts and splice variants of a transcriptome of a patient suffering
 CC from a particular disorder. ABN27253 to ABN59589 represent
 CC oligonucleotide sequences from rats, humans and mice, which are used in
 CC the exemplification of the present invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).
 XX
 SQ Sequence 60 BP; 15 A; 13 C; 15 G; 17 T; 0 other;
 XX
 Query Match 0.9%; Score 21.8; DB 24; Length 60;
 Best Local Similarity 61.4%; Pred. No. 7.1e+04;
 Matches 35; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
 XX
 QY 215 AACTTGCCATGAGACATTGTGAGAAATTTGAAATCTGAGAACTAGTGAACAGAG 271
 Db 59 AATTGGCCAGGCGACAGATGTTGCGACCTGTAATCTCAACATTTGAGACCAAG 3
 XX
 RESULT 78
 ABN50818
 ID ABN50818 standard; DNA; 60 BP.
 XX
 AC ABN50818;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Human spliced transcript detection oligonucleotide SEQ ID NO:23566.
 XX
 KW Human; mouse; rat; splice transcript; detection; RNA transcript;
 KW splice variant; transcriptome; oligonucleotide library; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200210449-A2.
 XX
 PD 07-FEB-2002.

```

XX 20-JUL-2001; 2001MO-IB01903.
PF
XX
XX 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
XX (COMP-) COMPUGEN INC.
XX
XX Shoshan A, Masserman A, Mintz E, Mintz L, Faigler S;
PI
XX WPI; 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes.
XX
XX Example 1; SEQ ID 23566; 47bp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the
XX (sub-)transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises
XX several oligonucleotides, each capable of hybridizing selectively to a
XX set of messenger RNAs transcribed from a given transcription unit of
XX the genome, which encodes one or more messenger RNA splice variants.
XX The oligonucleotide libraries are useful for detecting mRNAs from a
XX biological sample, in expression profiling studies, in qualitatively or
XX quantitatively characterizing the corresponding transcriptome, and in
XX detecting RNA transcripts and splice variants of human or animal
XX transcriptomes. The libraries may also be used as specialised mini
XX libraries to detect transcripts of a sub-transcriptome under a
XX particular biological or pathological state, and so allowing the
XX detection of tissue- and pathology-specific genes such as those genes
XX only expressed in specific tissue under a specific pathological
XX condition; to detect developmental specific genes; and to detect RNA
XX transcripts and splice variants of a transcriptome of a patient suffering
XX from a particular disorder. ABN27253 to ABN59589 represent
XX oligonucleotide sequences from rats, humans and mice, which are used in
XX the exemplification of the present invention.
XX N.B. The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 60 BP; 11 A; 12 C; 18 G; 19 T; 0 other;
SQ
XX
XX Query Match 0.9%; Score 21.8; DB 24; Length 60;
XX Best Local Similarity 65.3%; Pred. No. 7.1e+04;
XX Matches 32; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
XX
XX QY 1015 AGAATGCTCTCTCTGCTGGAGAGCTGCTGCGGAGCGCTGAGAG 1063
XX Db 3 AGAATGCTCTCTCTCTGAGGCGCTTCCTGAAACGAGTGTCAG 51
XX
XX RESULT 79
XX AAL30101/c
XX ID AAL30101 standard; DNA; 51 BP.
XX
XX AAL30101;
XX
XX 24-JAN-2002 (first entry)
XX
XX Human SNP oligonucleotide #3309.
XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
XX amyloid protein; angiotensin; apoptosis related protein; cadherin;
XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
XX complement related protein; cytochrome; kinase; cytokine; interferon;
XX interleukin; G-protein coupled receptor; thioesterase; inflammation;
XX multifactorial disease; autoimmune disease; infection;
XX nervous system disease; ss.
XX

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XX Homo sapiens.
OS
XX
XX MO200147944-A2.
PN
XX
XX 05-JUL-2001.
XX
XX 28-DEC-2000; 2000MO-US35498.
XX
XX 28-DEC-1999; 99US-0173419.
PR 27-DEC-2000; 2000US-0173419.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shinkets RA, Leach M;
PI
XX WPI; 2001-465210/50.
XX
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections.
XX
XX Claim 1; Page 2335; 4143bp; English.
XX
XX The present invention relates to oligonucleotides encoding polymorphic
XX variants of proteins related to amylases, amyloid proteins, angiotensin,
XX apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
XX histones, kinases, colony stimulating factors, complement related
XX proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
XX G-protein coupled receptors and thioesterases. The present sequence is
XX one such oligonucleotide. The oligonucleotides and the peptides encoded
XX by them may be used in the prevention, diagnosis and treatment of
XX diseases associated with inappropriate expression of the proteins listed
XX above. Disorders that may be prevented, diagnosed and/or treated include
XX multifactorial diseases with a genetic component, such as autoimmune
XX diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
XX systemic lupus erythematosus and Grave's disease), inflammation, cancer
XX (e.g. cancers of the bladder, brain, breast, colon and kidney,
XX leukemia), diseases of the nervous system and an infection of pathogenic
XX organisms.
XX
XX Sequence 51 BP; 10 A; 1 C; 4 G; 36 T; 0 other;
SQ
XX
XX Query Match 0.9%; Score 21.6; DB 22; Length 51;
XX Best Local Similarity 68.2%; Pred. No. 7.3e+04;
XX Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
XX
XX QY 1757 TTTAAATCAATCAATGCTGCAAAAAAACTTAAGCAAAA 1800
XX Db 45 TTTAAATCAATCAATGCTGCAAAAAAACTTAAGCAAAA 2
XX
XX RESULT 80
XX AAL30786/c
XX ID AAL30786 standard; DNA; 51 BP.
XX
XX AAL30786;
XX
XX 24-JAN-2002 (first entry)
XX
XX Human SNP oligonucleotide #3994.
XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
XX amyloid protein; angiotensin; apoptosis related protein; cadherin;
XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
XX complement related protein; cytochrome; kinase; cytokine; interferon;
XX interleukin; G-protein coupled receptor; thioesterase; inflammation;
XX multifactorial disease; autoimmune disease; infection;
XX nervous system disease; ss.
XX
XX Homo sapiens.
XX

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PN WO200147944-A2.
 XX
 PD 05-JUL-2001.
 XX
 PF 28-DEC-2000; 2000WO-US35498.
 XX
 PR 28-DEC-1999; 99US-0173419.
 PR 27-DEC-2000; 2000US-0173419.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkete RA, Leach M;
 XX
 DR WPI; 2001-465210/50.
 XX
 PT Polymorphic nucleic acids encoding e.g. amyloses, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -
 XX
 PS Claim 1; Page 2534; 4143pp; English.
 XX
 CC The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amyloses, amyloid proteins, angiotensin,
 CC apolipoprotein related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cyclochromes, kinesins, cytokines, interferons, interleukins,
 CC G-protein coupled receptors and thioesterases. The present sequence is
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded
 CC by them may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney, cancer
 CC leukaemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.
 CC
 SQ Sequence 51 BP; 8 A; 2 C; 3 G; 38 T; 0 other;
 XX
 QY Query Match 0.9%; Score 21.6; DB 22; Length 51;
 Best Local Similarity 68.2%; Pred. No. 7.3e+04;
 Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
 Db 1759 TAAATAATCATCATGTCGCAAAAAAACTTAAAGCAATA 1802
 46 TTAACATTAACATTCCTTAAAAAATAAAAAAAAAAAAAA 3
 RESULT 81
 AAI76504/c
 ID AAI76504 standard; DNA; 51 BP.
 XX
 AC AAI76504;
 XX
 DT 09-NOV-2001 (first entry)
 XX
 DE Human silent SNP containing nucleic acid SEQ:3445.
 XX
 KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
 KW protein therapy; vaccine; probe; diagnostic assay; detection;
 KW quantitation; restorative therapy; polymorphic; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200140521-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 30-NOV-2000; 2000WO-US32758.
 XX
 PR 30-NOV-1999; 99US-0168138.
 PR 29-NOV-2000; 2000US-0726173.
 PR

XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkete RA, Leach M;
 XX
 DR WPI; 2001-356160/37.
 XX
 PT Polymorphic nucleic acid sequences, useful in genetic testing and
 PT therapy -
 XX
 PS Claim 1; Page 1105; 2653pp; English.
 XX
 CC AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
 CC sequences (1), which contain single nucleotide polymorphisms (SNPs).
 CC AAI53114 to AAI53329 represent peptides related to human polymorphic
 CC polynucleotide sequences. The sequences can be used in gene and protein
 CC therapy, and in vaccine production. (1) and the polypeptides encoded by
 CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate expression of polymorphic polypeptides.
 CC For example, (1) may be used to treat disorders by rectifying mutations
 CC or deletions in a patient's genome that affect the activity of
 CC polypeptides by expressing inactive proteins or to supplement the
 CC patients own production of polypeptide. Additionally, (1) and its
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays to detect and quantitate the presence of similar nucleic acids
 CC in samples, and therefore which patients may be in need of restorative
 CC therapy. The polypeptides encoded by (1) may be used as antigens in the
 CC production of antibodies specific for polymorphic polypeptides. The
 CC antibodies may also be used to down regulate expression and activity.
 CC The antibodies may also be used as diagnostic agents for detecting the
 CC presence of polymorphic polypeptides in samples.
 CC
 SQ Sequence 51 BP; 13 A; 10 C; 5 G; 23 T; 0 other;
 XX
 QY Query Match 0.9%; Score 21.6; DB 22; Length 51;
 Best Local Similarity 68.2%; Pred. No. 7.3e+04;
 Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
 Db 1278 TGTACTTGAAGTGTGAAAGAAAGTTTCTTGAACCAAAA 1321
 45 TGTACTTGAAGTGTGAAAGTTTCTTGAACCAAAA 2
 RESULT 82
 AAI76505/c
 ID AAI76505 standard; DNA; 51 BP.
 XX
 AC AAI76505;
 XX
 DT 09-NOV-2001 (first entry)
 XX
 DE Human silent SNP containing nucleic acid SEQ:3446.
 XX
 KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
 KW protein therapy; vaccine; probe; diagnostic assay; detection;
 KW quantitation; restorative therapy; polymorphic; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200140521-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 30-NOV-2000; 2000WO-US32758.
 XX
 PR 30-NOV-1999; 99US-0168138.
 PR 29-NOV-2000; 2000US-0726173.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkete RA, Leach M;
 XX
 DR WPI; 2001-356160/37.
 DR

XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy -
XX

PS Claim 1, Page 1105; 2653pp; English.

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA153114 to AA153329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides.
CC For example, (I) may be used to treat disorders by rectifying mutations
CC or deletions in a patient's genome that affect the activity of
CC polypeptides by expressing inactive proteins or to supplement the
CC patients own production of polypeptide. Additionally, (I) and its
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids
CC in samples, and therefore which patients may be in need of restorative
CC therapy. The polypeptides encoded by (I) may be used as antigens in the
CC production of antibodies specific for polymorphic polypeptides. The
CC antibodies may also be used to down regulate expression and activity.
CC The antibodies may also be used as diagnostic agents for detecting the
CC presence of polymorphic polypeptides in samples.

SO Sequence 51 BP; 12 A; 10 C; 6 G; 23 T; 0 other;

Query Match 0.9%; Score 21.6; DB 22; Length 51;
Best Local Similarity 68.2%; Pred. No. 7.3e+04;
Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1278 TGTACTTGAAGTGTGAAGAAAGTTTCCTTGAACCAAAA 1321

Db 45 TGTACTTGAAGTGTGAAGTGTTCCTTGAAGCAAAA 2

RESULT 83
AA173964/c
ID AA173964 standard; cDNA to mRNA; 54 BP.

XX AA173964;

DT 27-AUG-1996 (first entry)

XX Human gene signature HUMGS05918.

XX Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW human; cloning; mapping; non-biased library; diagnosis; detection;
KW cell typing; abnormal cell function; ss.

XX Homo sapiens.

XX WO9514772-A1.

XX 01-JUN-1995.

XX 11-NOV-1994; 94MO-JP01916.

XX 12-NOV-1993; 93JP-0355504.

XX (MATS/) MATSUBARA K.

XX (OKUBO/) OKUBO K.

XX Matsubara K. Okubo K.

XX WPI; 1995-206931/27.

XX Identifying gene signatures in 3'-directed human cDNA library - e.g.
PT for diagnosis of abnormal cell function, by preparing cDNA that
PT reflects relative abundance of corresp. mRNA in specific human
XX tissues

PS Claim 1, Page 1497; 2245pp; Japanese.

XX A single-stranded DNA (or its complementary strand or the corresp.
CC double-stranded DNA) which comprises one of the 7837 "GS" sequences
CC given in AA119001-T26837 and which is able to hybridize to part of
CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
CC sequences were obtained from 3'-directed cDNA libraries prepared
CC from various human tissues; synthesis of cDNA was initiated from the
CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
CC untranslated sequence is unique to a particular mRNA species, almost
CC all the 3'-oriented cDNAs hybridize with specific mRNAs. Each library
CC is constructed so as to reflect accurately the relative abundance of
CC different mRNAs in the particular tissue from which it was derived.
CC The appearance frequency of a given GS in a cDNA library can be
CC determined (esp. using primers and probes derived from the GS
CC sequences) as a means of diagnosing abnormal cell function or for
CC recognising different cell types.

SO Sequence 54 BP; 19 A; 6 C; 8 G; 21 T; 0 other;

Query Match 0.9%; Score 21.6; DB 16; Length 54;
Best Local Similarity 63.5%; Pred. No. 7.5e+04;
Matches 33; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2086 TTTTACGTGCAACCAACCTGAATCTTTTATATATATATATATTTTCA 2137

Db 54 TTTGAGAGACGACCAAAATCAACCTTTATTTTATATAGTATATATGCA 3

RESULT 84
ABN36856
ID ABN36856 standard; DNA; 60 BP.

XX ABN36856;

DT 15-JUL-2002 (first entry)

XX Human spliced transcript detection oligonucleotide SEQ ID NO:9604.

XX Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.

XX Homo sapiens.

XX WO200210449-A2.

XX 07-FEB-2002.

XX 20-JUL-2001; 2001WO-1B01903.

XX 28-JUL-2000; 2000US-221607P.

XX 02-MAY-2001; 2001US-287724P.

XX (COMP-) COMPUGEN INC.

XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX WPI; 2002-257383/30.

XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes -

XX Example 1, SEQ ID 9604; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridizing selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.

CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcripts. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at http://www.wipo.int/pub/published_pct_sequences.

XX Sequence 60 BP; 22 A; 12 C; 18 G; 8 T; 0 other;

Query Match 0.9%; Score 21.6; DB 24; Length 60;

Best Local Similarity 63.5%; Pred. No. 8e+04; Indels 0; Gaps 0;

Matches 33; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Qy 245 AATCTCAGAACTAGTGTGAACAGAGGCGCAAAAATCAGACCAAGATG 296
Db 1 AAACGAGAGGAACCCATGATCCAGGCGGTGAAGATGAGAGCTACTG 52

RESULT 85
AAV69937
ID AAV69937 standard; DNA; 48 BP.

XX AAV69937;

XX 11-FEB-1999 (first entry)

XX Chlorella virus promoter consensus sequence cyp-6.

XX Promoter; Chlorella virus; structural gene; lac operon;
XX protein expression; ss.

XX Chlorella sp.

XX WO9842822-A1.

XX 01-OCT-1998.

XX 21-MAR-1998; 98WO-US05655.

XX 21-MAR-1997; 97US-0821559.

XX (BION-) BIONEERASKA INC.

XX xia y;

XX WPI; 1998-609893/51.

PT Promoter sequences derived from Chlorella virus - are useful for
PT heterologous protein production in plants

XX Example 6; Page 15; 46pp; English.

CC AAV69935-46 represent promoter consensus sequences. The specification
CC describes promoter sequences derived from Chlorella virus. These
CC promoter sequences direct transcription of a structural gene. A lac
CC operon can be linked operatively to the promoters. The promoters can
CC be used in constructs for promoting high level expression of proteins
CC e.g. heterologous proteins, in a host, especially plants such tobacco,
CC wheat.

XX Sequence 48 BP; 17 A; 7 C; 9 G; 15 T; 0 other;

Query Match 0.9%; Score 21.4; DB 19; Length 48;
Best Local Similarity 66.0%; Pred. No. 8e+04;
Matches 31; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
Qy 223 CTTCCTGGGAATATATATGCAATGATCATGTTACACA 2279
Db 2 CTATCGTGTGATGATATATGACAAATGATGCTGATCAACA 48

RESULT 86

AA521106
ID AA521106 standard; DNA; 48 BP.

XX AA521106;

XX 20-MAR-2002 (first entry)

XX (GGA)16 DNA purification oligonucleotide.

XX ss; DNA purification; triple helix; plasmid purification.

XX Synthetic.

XX Key Location/Qualifiers

FT repeat_region 1..48

FT /tag= a

FT /rpt_type= "TANDEM"

FT repeat_unit 1..3

FT /tag= b

FT /note= "GAA repeat type"

XX WO200192511-A2.

XX 06-DEC-2001.

XX 25-MAY-2001; 2001WO-US17122.

XX 26-MAY-2000; 2000US-0580923.

XX (AVET) AVENTIS PHARMA SA.

XX Crouzet J, Scherman D, Wils P, Blanche F, Cameron B;

XX WPI; 2002-097772/13.

XX This invention comprises a method of purifying double-stranded DNA from

XX a solution containing the double-stranded DNA mixed with other

XX components, comprising passing the solution through a support comprising

XX a covalently coupled oligonucleotide capable of forming a triple helix

XX with the double-stranded DNA by hybridisation with a specific purifying

XX present in the double-stranded DNA. The method is useful for purifying

XX double-stranded DNA contained in a solution and mixed with other

XX components. The new method is a simple, rapid and effective method for

XX DNA purification, and makes it possible to obtain especially high

XX purities with high yields. The method enables DNA to be purified from

XX complex mixtures comprising other nucleic acids, proteins, endotoxins,
XX nucleases and the like. The supports may be readily recycled, and the
XX DNAs obtained display improved properties to pharmaceutical safety.
XX Further, the method entails only one step contrary to prior art.
XX The present sequence represents a DNA sequence contained within the
XX plasmid pXL2725. This sequence is used for purification of this
XX plasmid using the method of the invention.

XX Sequence 48 BP; 16 A; 0 C; 32 G; 0 U; 0 other;

Query Match 0.9%; Score 21.4; DB 24; Length 48;

Best Local Similarity 66.0%; Pred. No. 8e+04;
Matches 31; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 123 GGACCCAGCAGAGACCGGCTCTGAGATGAGCTGAGAGAGGCGG 169
DB 1 GGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 47

RESULT 87
AAD24852
ID AAD24852 standard; DNA; 48 BP.
AC AAD24852;
XX
XX 12-MAR-2002 (first entry)
XX
XX Chlorella virus cyp-6 promoter DNA consensus.
DE
XX
XX Gene expression; heterologous enzyme; hormone; structural protein;
KW Escherichia coli cell; tobacco; wheat; ds.
XX
XX Chlorella virus.
OS
XX US6316224-B1.
PN
XX 13-NOV-2001.
PD
XX 21-SEP-1999; 99US-0400541.
PF
XX 21-MAR-1997; 97US-0821559.
PR 21-MAR-1998; 98WO-US05655.
XX
XX (BION-) BIONEERASRA INC.
PA
XX
PI Xia Y;
XX
XX WPI; 2002-054589/07.
DR
XX
XX Chlorella virus promoters, useful for controlling expression of
PT hormones, enzymes and structural proteins in plant and Escherichia coli
PT cells -
XX
XX
XX Example 6; Column 9-10; 24pp; English.
PS
XX The invention relates to isolated, inducible promoter sequences derived
CC from Chlorella viruses. The invention also relates to gene constructs
CC comprising a promoter sequence of the invention operably linked to a DNA
CC sequence of a structural gene. The promoter is used for controlling gene
CC expression in host cells. In particular, it is used for control expression
CC of genes encoding heterologous enzymes, hormones, structural proteins,
CC glucagon-like peptide 1, growth hormone releasing factor, parathyroid
CC hormone, carbonic anhydrase, beta-galactosidase, chloramphenicol acetyl
CC transferase or glutathione acetyltransferase in plants cells and
CC Escherichia coli cells. The promoters can also promote high levels of
CC expression in plants especially tobacco and wheat. The present sequence
CC is Chlorella virus cyp-6 promoter DNA consensus.
XX
XX Sequence 48 BP; 17 A; 7 C; 9 G; 15 T; 0 other;

Query Match 0.9%; Score 21.4; DB 24; Length 48;
Best Local Similarity 66.0%; Pred. No. 8e+04;
Matches 31; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 2233 CTCTCTTGGTGAATTAATGAATGCAATGATCATTTTAACA 2279
DB 2 CTATATCGTTGATATGATAAATGACAAATGATACGCTGATACACA 48

RESULT 88
AAL31468
ID AAL31468 standard; DNA; 51 BP.
XX
XX AAL31468;

XX 24-JAN-2002 (first entry)
DT
XX
XX Human SNP oligonucleotide #4676.
DE
XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinase; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
XX Homo sapiens.
OS
XX
XX W0200147944-A2.
PN
XX
XX 05-JUL-2001.
PD
XX
XX 28-DEC-2000; 2000WO-US35498.
PF
XX
XX 28-DEC-1999; 99US-0173419.
PR 27-DEC-2000; 2000US-0173419.
XX
XX (CURA-) CURAGEN CORP.
PA
XX
XX Shimketa RA, Leach M;
PI
XX
XX WPI; 2001-465210/50.
DR
XX
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -
XX
XX Claim 1; Page 2731; 4143pp; English.
PS
XX
XX The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukemia), diseases of the nervous system and an infection of pathogenic
CC organisms.
XX
XX Sequence 51 BP; 13 A; 6 C; 6 G; 26 T; 0 other;

Query Match 0.9%; Score 21.4; DB 22; Length 51;
Best Local Similarity 80.6%; Pred. No. 8.3e+04;
Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2100 AACCTGATCTTTTATATATAATATA 2130
DB 4 AACCAAGATCTTTTATATATCTGTA 34

RESULT 89
AAL78865/C
ID AAL78865 standard; DNA; 51 BP.
XX
XX AAL78865;
AC
XX 09-NOV-2001 (first entry)
DT
XX

PS Claim 1; SEQ ID 15425; 71bp + CD-ROM; English.

XX The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNA or poly(A) RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.

SQ Sequence 59 BP; 22 A; 8 C; 8 G; 21 T; 0 other;

Query Match 0.9%; Score 21.4; DB 21; Length 59;
Best Local Similarity 66.0%; Pred. No. 8.9e+04;
Matches 31; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 2090 AGCTGCAACACCTGAACTCTTTTATATATAATATATTTTC 2136
DB 10 ACATTGATGCAACGCTATTTTATATATAATATATATACGTCTC 56

RESULT 92
ABN32960/c
ID ABN32960 standard; DNA; 60 BP.
XX
AC ABN32960;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:5708.
XX
KM Human; mouse; rat; splice transcript; detection; RNA transcript;
XX splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN MO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WC-IB01903.
XX
PR 28-JUL-2000; 2000US-221607P.
XX 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
XX selectively hybridize to mRNAs transcribed from a transcription unit of
XX a genome, useful for detecting tissue-, pathology-, and
XX developmental-specific genes
XX
PS Example 1; SEQ ID 5708; 47bp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the
XX (sub-)transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises
XX several oligonucleotides, each capable of hybridising selectively to a
XX set of messenger RNAs transcribed from a given transcription unit of
XX the genome, which encodes one or more messenger RNA splice variants.
XX The oligonucleotide libraries are useful for detecting mRNAs from a

CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN55589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 60 BP; 16 A; 11 C; 13 G; 20 T; 0 other;

Query Match 0.9%; Score 21.4; DB 24; Length 60;
Best Local Similarity 66.0%; Pred. No. 9e+04;
Matches 31; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 2174 CCAACTTTAAATGCGAAATATGCTTGCTGTAAGAAAGCCAGA 2220
DB 59 CCAAGTTTCATTATCATGCAATCGCTTGCTGCAAGAAAGCCAGA 13

RESULT 93
ABN37046
ID ABN37046 standard; DNA; 60 BP.
XX
AC ABN37046;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:9794.
XX
KM Human; mouse; rat; splice transcript; detection; RNA transcript;
XX splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN MO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WC-IB01903.
XX
PR 28-JUL-2000; 2000US-221607P.
XX 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
XX selectively hybridize to mRNAs transcribed from a transcription unit of
XX a genome, useful for detecting tissue-, pathology-, and
XX developmental-specific genes
XX
PS Example 1; SEQ ID 9794; 47bp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the
XX (sub-)transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises
XX several oligonucleotides, each capable of hybridising selectively to a
XX set of messenger RNAs transcribed from a given transcription unit of
XX the genome, which encodes one or more messenger RNA splice variants.
XX The oligonucleotide libraries are useful for detecting mRNAs from a

CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 60 BP; 16 A; 12 C; 14 G; 18 T; 0 other;
SQ

Query Match 0.9%; Score 21.4; DB 24; Length 60;
Best Local Similarity 71.8%; Pred. No. 9e+04;
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 1256 GTTTACATATGTCGCTCCATCTGACTTGAAGTGCA 1294
Db 9 GTTACATTCAGGCACTATGTGAAGTGA 47

RESULT 94
ABN37096/c
ID ABN37096 standard; DNA; 60 BP.
XX
AC ABN37096;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:9844.
XX
KM Human; mouse; rat; splice transcript; detection; RNA transcript;
KM splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB01903.
XX
PR 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
PI WPI; 2002-257383/30.
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes
XX
PS Example 1; SEQ ID 9844; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the
XX (sub-)transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises
XX several oligonucleotides, each capable of hybridising selectively to a
XX set of messenger RNAs transcribed from a given transcription unit of
XX the genome, which encodes one or more messenger RNA splice variants.
XX The oligonucleotide libraries are useful for detecting mRNAs from a

CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 60 BP; 15 A; 17 C; 13 G; 15 T; 0 other;
SQ

Query Match 0.9%; Score 21.4; DB 24; Length 60;
Best Local Similarity 66.0%; Pred. No. 9e+04;
Matches 31; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 1011 GAAAGAAATGCTCTCTCTGAGAGCTGCTCGGAGAGCTG 1057
Db 47 GAAAGAAATGCTCTCTCTGAGAGCTGCTCGGAGAGCAATG 1

RESULT 95
ABN50863/c
ID ABN50863 standard; DNA; 60 BP.
XX
AC ABN50863;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:23611.
XX
KM Human; mouse; rat; splice transcript; detection; RNA transcript;
KM splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB01903.
XX
PR 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
PI WPI; 2002-257383/30.
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes
XX
PS Example 1; SEQ ID 23611; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the
XX (sub-)transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises
XX several oligonucleotides, each capable of hybridising selectively to a
XX set of messenger RNAs transcribed from a given transcription unit of
XX the genome, which encodes one or more messenger RNA splice variants.
XX The oligonucleotide libraries are useful for detecting mRNAs from a

CC biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterizing the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcripts. The libraries may also be used as specialised mini
 CC libraries to detect transcripts of a sub-transcriptome under a
 CC particular biological or pathological state, and so allowing the
 CC detection of tissue- and pathology-specific genes such as those genes
 CC only expressed in specific tissue under a specific pathological
 CC condition; to detect developmental specific genes; and to detect RNA
 CC transcripts and splice variants of a transcriptome of a patient suffering
 CC from a particular disorder. ABN27253 to ABN59589 represent
 CC oligonucleotide sequences from rats, humans and mice, which are used in
 CC the exemplification of the present invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 60 BP, 20 A, 15 C, 11 G, 14 T, 0 other;

Query Match 0.9%; Score 21.4; DB 24; Length 60;
 Best Local Similarity 71.8%; Pred. No. 9e+04; Mismatches 0; Gaps 0;
 Matches 28; Conservative 0; Indels 11;

OY 2191 AAATTATGTTGGTGTGAGAGAAAGCCAGACACTTCTG 2229
 39 AAATGATGGGTCTATGAGAGATAGCCTGATAGCCTCTG 1

RESULT 96
 AAH44690/c
 ID AAH44690 standard; DNA; 41 BP.
 XX
 AC AAH44690;
 XX
 DT 07-DEC-2001 (first entry)
 XX
 DE Human type-I aminoacyl tRNA synthetase 10 probe 1 SEQ ID NO:8.
 XX
 KM Human; type-I aminoacyl tRNA synthetase 10; malignant tumour;
 KM haemopathy; human immunodeficiency virus; HIV infection;
 KM immunological disease; inflammation; probe; ss.
 XX
 OS Homo sapiens.
 XX
 PN CN1301715-A.
 XX
 PD 04-JUL-2001.
 XX
 PF 27-DEC-1999; 99CN-0125371.
 XX
 PR 27-DEC-1999; 99CN-0125371.
 XX
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2001-550469/62.
 XX
 PT New polypeptide-I-type aminoacyl-tRNA synthetase 10 and encoding
 PT polynucleotide useful for treating tumor, hemopathy, infection and
 PT immunological disease -
 XX
 PS Example 7; Page 20 (Disclosure); 32pp; Chinese.
 XX
 CC The present invention describes the human type-I aminoacyl tRNA
 CC synthetase 10 protein. Also described are polynucleotides encoding the
 CC type-I aminoacyl tRNA synthetase 10 protein, and a DNA recombination
 CC process to produce the protein. The protein can be used for treating
 CC various diseases, such as malignant tumour, haemopathy, human
 CC immunodeficiency virus infection, immunological diseases and various
 CC inflammations. The present sequence represents a probe for type-I
 CC aminoacyl tRNA synthetase 10, which is used in an example from the
 CC present invention.

XX
 SQ Sequence 41 BP, 3 A, 5 C, 3 G, 30 T, 0 other;

Query Match 0.9%; Score 21.2; DB 22; Length 41;
 Best Local Similarity 76.5%; Pred. No. 8.4e+04;
 Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 2045 AAAATGGAGGCGAAGACAAAGAACTTACCA 2078
 37 AAAAAGAAAAGAAAAGAAAAGAACTTACCA 4

RESULT 97
 AAF29312/c
 ID AAF29312 standard; DNA; 48 BP.
 XX
 AC AAF29312;
 XX
 DT 18-APR-2001 (first entry)
 XX
 DE Primer base sequence used to illustrate primer selection method.
 XX
 KM Primer; optimum sequence; differential display; ss.
 XX
 OS Synthetic.
 XX
 PN JP2000308487-A.
 XX
 PD 07-NOV-2000.
 XX
 PF 30-MAR-1999; 99JP-0088410.
 XX
 PR 30-MAR-1999; 99JP-0088410.
 XX
 PA (KAGAKU GIUTSU SHINKO JIGYODAN.
 XX
 DR WPI; 2001-046077/06.
 XX
 PT Selection of primer base for optimizing primer selection comprises
 PT obtaining an optimum sequence for differential display from an
 PT expression gene data base -
 XX
 PS Disclosure; Fig 9; 13pp; Japanese.
 XX
 CC This invention relates to a method for selecting the sequence of a
 CC primer. The method comprises obtaining an optimum sequence for
 CC differential display from an expression gene data base, and using the
 CC base sequences most frequently expressed as the primer candidates in the
 CC order of frequency. The optimum primer group characterised by the use of
 CC genetic algorithm from the primer candidates is selected. The method is
 CC used for selecting a primer used in an illustration of the present sequence
 CC represents a primer used in an illustration of the method of the
 CC invention.

SQ Sequence 48 BP, 18 A, 2 C, 5 G, 23 T, 0 other;

Query Match 0.9%; Score 21.2; DB 22; Length 48;
 Best Local Similarity 69.0%; Pred. No. 9e+04; Mismatches 13; Indels 0; Gaps 0;
 Matches 29; Conservative 0;

OY 2097 AACACCTGAATCTTTTATATATAATATATTTTCAA 2138
 47 AAGAAATTGAATCTTCAATTTTAAAAAAAATTCTTCAA 6

RESULT 98
 AA177361/c
 ID AA177361 standard; DNA; 50 BP.
 XX
 AC AA177361;
 XX
 DT 09-NOV-2001 (first entry)
 XX

DE		Human silent SNP containing nucleic acid SEQ:4302.
XX		
KM		Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW		protein therapy; vaccine; probe; diagnostic assay; detection;
OS		quantitation; restorative therapy; polymorphic; ds.
XX		
XX	Homo sapiens.	
FN	WO200140521-A2.	
PD	07-JUN-2001.	
PF	30-NOV-2000; 2000MO-US32758.	
FR	30-NOV-1999; 98US-0168138.	
XX	29-NOV-2000; 2000US-0726173.	
PA	(CURA-) CURAGEN CORP.	
PI	Shimkets RA, Leach M;	
DR	WPI; 2001-356160/37.	
PT	Polymorphic nucleic acid sequences, useful in genetic testing and therapy -	
PS	Claim 1; Page 1827; 2653jp; English.	
XX	AAT73060 to AAT79867 represent isolated human polymorphic polynucleotide sequences (I), which contain single nucleotide polymorphisms (SNPs).	
CC	AAM53114 to AAM53129 represent peptides related to human polymorphic polynucleotide sequences. The sequences can be used in gene and protein therapy, and in vacine production. (I) and the polypeptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of polymorphic polypeptides. For example, (II) may be used to treat disorders by rectifying mutations or deletions in a patient's genome that affect the activity of polypeptides by expressing inactive proteins or to supplement the patients own production of polypeptide. Additionally, (I) and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The polypeptides encoded by (I) may be used as antigens in the production of antibodies specific for polymorphic polypeptides. The antibodies may also be used to down regulate expresion and activity. The antibodies may also be used as diagnostic agents for detecting the presence of polymorphic polypeptides in samples.	
SQ	Sequence 50 BP; 12 A; 13 C; 7 G; 18 T; 0 other;	
Query Match	0.9%; Score 21.2; DB 22; Length 50;	
Best Local Similarity	69.0%; Pred.No.9.2e+04;	
Matches	29; Conservative 0; MisMatches 13; Indels 0; Gaps 0;	
DY	895 GCACCCCCTTCAGTGGGGAATAAGAAAGAACAATTGAC 936	
DB	46 GCATACCATTACTCGGGGGAAAAAAAAGTTTAAGAGATGCC 5	
RESULT 99		
AAA77364/C		
ID	AAA77364 standard; cDNA; 51 BP.	
XX	AAA77364;	
DT	16-NOV-2000 (first entry)	
DE	Human clone CG44911913 polymorphic site, SEQ ID NO:1047.	
XX	Human; single nucleotide polymorphism; SNP; chromosome 15;	
KW	detection; identification; gene therapy; ss.	
OS	Homo sapiens.	

[illegible]

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ALIGNMENTS

```
RESULT 1
US-09-461-697-231
; Sequence 231, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COCENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461,697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-697-231

Query Match      1.0%; Score 23.6; DB 4; Length 60;
Best Local Similarity 64.8%; Pred. No. 2.1e+03;
Matches 35; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1635 AAAAAGTGGAGGAGAGATGTGAGCATCTGCAAGTGAACAACACTCAA 1688
DB 7 AAGAAGATGAAGTGGAAATGAGGAAGAGCTGGAAAAGAGAAGATTAA 60

RESULT 2
US-08-198-094-72
; Sequence 72, Application US/08198094
; Patent No. 5741696
; GENERAL INFORMATION:
; APPLICANT: Cochran Ph.D., Mark D
; TITLE OF INVENTION: Recombinant Equine Herpesvirus
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/198,094
; FILING DATE: February 17, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)977-9550
; TELEFAX: (212)664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Equine Herpesvirus
PCT-US95-02087-72

Query Match      1.0%; Score 23.4; DB 5; Length 54;
Best Local Similarity 67.3%; Pred. No. 2.3e+03;
Matches 33; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
```

```
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Equine Herpesvirus
US-08-198-094-72

Query Match      1.0%; Score 23.4; DB 1; Length 54;
Best Local Similarity 67.3%; Pred. No. 2.3e+03;
Matches 33; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 760 CATGATGACAGTCACACACATTTTGTGGAACATAGATACATGCG 808
DB 1 CCTATGTATCATACATACATGATTGAGTGACACTTATGAAATACCGG 49

RESULT 3
PCT-US95-02087-72
; Sequence 72, Application PC/TUS9502087
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D
; TITLE OF INVENTION: Recombinant Equine Herpesviruses
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/198,094
; FILING DATE: February 17, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278-0400
; TELEFAX: (212)391-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Equine Herpesvirus
PCT-US95-02087-72

Query Match      1.0%; Score 23.4; DB 5; Length 54;
Best Local Similarity 67.3%; Pred. No. 2.3e+03;
Matches 33; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
```


NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02736
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 162:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-08-823-516-162

Query Match 1.0%; Score 22.6; DB 2; Length 54;
Best Local Similarity 75.7%; Pred. No. 3.7e+03;
Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 128 AGCAGAGAGCGGGCTCTGAGATGAGCTGAGAGA 164
DB 4 AGAAGAGAGAGGGGTCTCTGAGAGAGCGGAGAGA 40

RESULT 7

US-08-171-389-63
Sequence 63, Application US/08171389
Patent No. 5578444
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSER: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,389
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human sodium/potassium ATPase alpha
INDIVIDUAL ISOLATE: 3 subunit (ATP1 A3)
US-08-171-389-63

Query Match 1.0%; Score 22.4; DB 1; Length 44;
Best Local Similarity 72.5%; Pred. No. 3.8e+03;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 9 CTGCGCGGGTCCGGGCCATGAGCGACGAGAGGCGCG 48
DB 4 CTCCTCGGACGCGGCGCATATGAGAGCGGAGCGCGCG 43

RESULT 8

US-08-123-936-63
Sequence 63, Application US/08123936
Patent No. 5726014
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
TITLE OF INVENTION: Screening Assay for the Detection of
TITLE OF INVENTION: DNA-Binding Molecules
NUMBER OF SEQUENCES: 640
CORRESPONDENCE ADDRESS:
ADDRESSER: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,936
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0075.32/G19P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human sodium/potassium ATPase alpha

INDIVIDUAL ISOLATE: 3 subunit (ATP1 A3)
US-08-123-936-63

Query Match 1.0%; Score 22.4; DB 1; Length 44;
Best Local Similarity 72.5%; Pred. No. 3.8e+03;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 9 CTGCGCGGCTCCGGCCCATGAGCGGACGAGAGGCGCG 48
DB 4 CTCCCGCGGACGCGGGCATATGAGAGCGGAGCGGCGG 43

RESULT 9

US-08-475-228A-63
Sequence 63, Application US/08475228A
Patent No. 5869241

GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.

APPLICANT: Cantor, Charles R.

APPLICANT: Andrews, Beth M.

APPLICANT: Turin, Lisa M.

TITLE OF INVENTION: Sequence-Directed DNA Binding

NUMBER OF SEQUENCES: 664

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.

STREET: 505 Penobscot Drive

CITY: Redwood City

STATE: CA

COUNTRY: USA

ZIP: 94063

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,228A

FILING DATE: 06-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936

FILING DATE: 17-SEP-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783

FILING DATE: 23-DEC-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618

FILING DATE: 27-JUN-1991

APPLICATION NUMBER: US 08/081,070

ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.

REGISTRATION NUMBER: 34,444

REFERENCE/DOCKET NUMBER: 4600-0175.21/G19P3D2

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human sodium/potassium ATPase alpha
INDIVIDUAL ISOLATE: 3 subunit (ATP1 A3)
US-08-475-228A-63

Query Match 1.0%; Score 22.4; DB 2; Length 44;

Best Local Similarity 72.5%; Pred. No. 3.8e+03;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 9 CTGCGCGGCTCCGGCCCATGAGCGGACGAGAGGCGCG 48
DB 4 CTCCCGCGGACGCGGGCATATGAGAGCGGAGCGGCGG 43

RESULT 10

US-08-482-080A-63
Sequence 63, Application US/08482080A
Patent No. 6010849

GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.

APPLICANT: Cantor, Charles R.

APPLICANT: Andrews, Beth M.

APPLICANT: Turin, Lisa M.

TITLE OF INVENTION: Sequence-Directed DNA Binding

NUMBER OF SEQUENCES: 664

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.

STREET: 505 Penobscot Drive

CITY: Redwood City

STATE: CA

COUNTRY: USA

ZIP: 94063

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,080A

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/171,389

FILING DATE: 20-DEC-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936

FILING DATE: 17-SEP-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783

FILING DATE: 23-DEC-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618

FILING DATE: 27-JUN-1991

APPLICATION NUMBER: US 08/081,070

ATTORNEY/AGENT INFORMATION:
NAME: Brady, John F.

REGISTRATION NUMBER: 39,118

REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880

TELEFAX: (650) 324-0960

INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human sodium/potassium ATPase alpha
INDIVIDUAL ISOLATE: 3 subunit (ATP1 A3)
US-08-482-080A-63

Query Match 1.0%; Score 22.4; DB 3; Length 44;
Best Local Similarity 72.5%; Pred. No. 3.8e+03;

Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 9 CTGGGGGGGTCCTCGGGCCCATGAGCGAGCGAGGCGG 48
DB 4 CTCCCGCGACGCGGCGCATATGAGAGCGGAGCGGCGG 43

RESULT 11

US-09-354-947-63

Sequence 63, Application US/09354947

Patent No. 6384208

GENERAL INFORMATION:

APPLICANT: Edwards, Cynthia A.

APPLICANT: Cantor, Charles R.

APPLICANT: Andrews, Beth M.

APPLICANT: Turin, Lisa M.

APPLICANT: Fly, Kirk E.

TITLE OF INVENTION: Sequence-Directed DNA Binding

TITLE OF INVENTION: Molecules, Compositions and Methods

NUMBER OF SEQUENCES: 664

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genelabs Technologies, Inc.

STREET: 505 Penobscot Drive

CITY: Redwood City

STATE: CA

COUNTRY: USA

ZIP: 94063

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/354,947

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/482,080

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/171,389

FILING DATE: 20-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/123,936

FILING DATE: 17-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/996,783

FILING DATE: 23-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/723,618

FILING DATE: 27-JUN-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/081,070

FILING DATE: 22-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Brady, John F.

REGISTRATION NUMBER: 39,118

REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 324-0880

TELEFAX: (650) 324-0960

INFORMATION FOR SEQ ID NO: 63:

SEQUENCE CHARACTERISTICS:

LENGTH: 44 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHEICAL: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: Human sodium/potassium ATPase alpha

INDIVIDUAL ISOLATE: 3 subunit (ATP1 A3)

US-09-354-947-63

Query Match 1.0%; Score 22.4; DB 4; Length 44;

Best Local Similarity 72.5%; Pred. No. 3.8e+03;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 9 CTGGGGGGGTCCTCGGGCCCATGAGCGAGCGAGGCGG 48
DB 4 CTCCCGCGACGCGGCGCATATGAGAGCGGAGCGGCGG 43

RESULT 12

PCT-US93-12388-63

Sequence 63, Application PC/TUS9312388

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Sequence-Directed DNA Binding

TITLE OF INVENTION: Molecules, Compositions and Methods

NUMBER OF SEQUENCES: 641

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genelabs Technologies, Inc.

STREET: 505 Penobscot Drive

CITY: Redwood City

STATE: CA

COUNTRY: USA

ZIP: 94063

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/12388

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/123,936

FILING DATE: 17-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/996,783

FILING DATE: 23-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: Fabian, Gary R.

REGISTRATION NUMBER: 33,875

REFERENCE/DOCKET NUMBER: 4600-0175.41/G19PCT2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 63:

SEQUENCE CHARACTERISTICS:

LENGTH: 44 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHEICAL: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: Human sodium/potassium ATPase alpha

INDIVIDUAL ISOLATE: 3 subunit (ATP1 A3)

PCT-US93-12388-63

Query Match 1.0%; Score 22.4; DB 5; Length 44;
Best Local Similarity 72.5%; Pred. No. 3.8e+03;

Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 9 CTGGGGGGGTCCTCGGGCCCATGAGCGAGCGAGGCGG 48
DB 4 CTCCCGCGACGCGGCGCATATGAGAGCGGAGCGGCGG 43

RESULT 13

US-08-171-389-212

Sequence 212, Application US/08171389

Patent No. 5578444

GENERAL INFORMATION:

APPLICANT: Edwards, Cynthia A.

APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk B.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSER: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,389
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 212:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human interleukin 4 gene
US-08-171-389-212
Query Match 0.9%; Score 22.2; DB 1; Length 45;
Best Local Similarity 77.1%; Pred. No. 4.4e+03;
Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 933 TGACAAATCTCAATGTAACTCAATTGCTC 967
DB 9 TAAAGAAATTTCCAAATGTAACTCAATTGCTC 43
RESULT 14
US-08-123-936-212
Sequence 212, Application US/08123936
Patent No. 5726014
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
TITLE OF INVENTION: Screening Assay for the Detection of

TITLE OF INVENTION: DNA-Binding Molecules
NUMBER OF SEQUENCES: 640
CORRESPONDENCE ADDRESS:
ADDRESSER: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,936
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0075.32/G19P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 212:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human interleukin 4 gene
US-08-123-936-212
Query Match 0.9%; Score 22.2; DB 1; Length 45;
Best Local Similarity 77.1%; Pred. No. 4.4e+03;
Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 933 TGACAAATCTCAATGTAACTCAATTGCTC 967
DB 9 TAAAGAAATTTCCAAATGTAACTCAATTGCTC 43
RESULT 15
US-08-475-228A-212
Sequence 212, Application US/08475228A
Patent No. 5869241
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk B.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSER: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,228A
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 4600-0175.21/G19P3D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 212:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human interleukin 4 gene
US-08-475-228A-212

Query Match 0.9%; Score 22.2; DB 2; Length 45;
Best Local Similarity 77.1%; Pred. No. 4.4e+03;
Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 933 TGACAAATCTCAATGTAACTCAATTGCGCTC 967
Db 9 TAAAGAAATTTCATGTAACTCAATTGCGCTC 43

RESULT 16
US-08-482-080A-212
Sequence 212, Application US/08482080A
Patent No. 6010849
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/482,080A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/171,389
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Brady, John F.
REGISTRATION NUMBER: 39,118
REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 212:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human interleukin 4 gene
US-08-482-080A-212

Query Match 0.9%; Score 22.2; DB 3; Length 45;
Best Local Similarity 77.1%; Pred. No. 4.4e+03;
Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 933 TGACAAATCTCAATGTAACTCAATTGCGCTC 967
Db 9 TAAAGAAATTTCATGTAACTCAATTGCGCTC 43

RESULT 17
US-09-354-947-212
Sequence 212, Application US/09354947
Patent No. 6384208
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/354,947
FILING DATE:

PRIOR APPLICATION DATA: US 08/482,080
 APPLICATION NUMBER: US 08/482,080
 FILING DATE: 07-JUN-1995
 APPLICATION NUMBER: US 08/171,389
 FILING DATE: 20-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/123,936
 FILING DATE: 17-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/996,783
 FILING DATE: 23-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/723,618
 FILING DATE: 27-JUN-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/081,070
 FILING DATE: 22-JUN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Brady, John F.
 REGISTRATION NUMBER: 39,118
 REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 324-0880
 TELEFAX: (650) 324-0960
 INFORMATION FOR SEQ ID NO: 212:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 45 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHEetical: NO
 ORIGINAL SOURCE: Human interleukin 4 gene
 IS-09-354-947-212

Query Match	0.9%	Score 22.2;	DB 4;	Length 45;
Best Local Similarity	77.1%	Pred. No. 4.4e+03;		
Matches 27; Conservative	0;	Mismatches 8;	Indels 0;	Gaps 0;

Qy	933	TGACAAATCTCAATGTAACTCAATTTGCCTC	96
Db	9	TAACGAAATTTCAATGTAACTCATTTCCCTC	43

RESULT 18
PCT-US93-12388-212

```
; Sequence 212, Application PC/TUS9312388
; GENERAL INFORMATION:
```

1	APPLICANT:	Sequence-Directed DNA Binding
2	TITLE OF INVENTION:	Molecules, Compositions and Methods
3	TITLE OF INVENTION:	Molecules, Compositions and Methods
4	NUMBER OF SEQUENCES:	641

! CORRESPONDENCE ADDRESS:
! ADDRESSEE: Genelabs Technologies, Inc.

STREET: 505 Penobscot Drive
CITY: Redwood City

STATE: CA
COUNTRY: USA
STD: 04063

ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: 510000

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS

```

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

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APPLICATION NUMBER: PCT/US93/123888
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION

APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/996,783
 FILING DATE: 23-DEC-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Fabian, Gary R.
 REGISTRATION NUMBER: 33,875
 REFERENCE/DOCKET NUMBER: 4600-0175.41/G19PCT22
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 212:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 45 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: Human interleukin 4 gene

Query Match	0.9%	Score 22.2	DB 5	Length 45
Best Local Similarity	77.1%	Pred. NO. 4.4e+03		
Matches 27	Conservative	0	Mismatches 8	Indels 0
				Gaps 0

Qy	933	TGACAAATCTCTAAATGTAACTCAATTGCCTC	967
Db	9	TAACGAAATTTCCATGTAACTCATTTTCCCTC	43

RESULT 19
US-09-641-638-880/c
; Sequence 880, Application US/09641638

; Patent No. 6432648
; GENERAL INFORMATION:

! APPLICANT: Blumenfeld, Marta
! APPLICANT: Bougueleret, Lydie

APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Annick

1 TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
2
3
4 TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
5
6
7 TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
8
9
10 TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
11
12
13 TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
14
15
16 TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
17
18
19 TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
20
21
22 TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
23
24
25 TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
26
27
28 TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
29
30
31 TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
32
33
34 TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
35
36
37 TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
38
39
40 TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
41
42
43 TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
44
45
46 TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
47
48
49 TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
50
51
52 TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
53
54
55 TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
56
57
58 TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
59
60
61 TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
62
63
64 TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
65
66
67 TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
68
69
70 TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
71
72
73 TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
74
75
76 TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
77
78
79 TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
80
81
82 TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
83
84
85 TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
86
87
88 TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
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91 TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
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94 TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
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97 TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
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100 TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM

FILE REFERENCE: GENSEI.051CPI
CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000 08 16

;; CURRENT FILING DATE: 2000-08-16
;; PRIOR APPLICATION NUMBER: US 09/502,330
;; PRIOR FILING DATE: 2000-03-11

PRIOR FILING DATE: 2000-02-11
 PRIOR APPLICATION NUMBER: US 60/133,200
 PRIOR FILING DATE: 1999-05-07

PRIOR FILING DATE: 1999-03-23

PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12

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: NUMBER OF SEQ ID NOS: 1304
:
: SOFTWARE: Patent.pm
:

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; SEQ ID NO 880
;
; LENGTH: 47

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; TYPE: DNA
; ORGANISM: Homo Sapiens

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; FEATURE:
; NAME/KEY: allele
;
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LOCATION: 24
OTHER INFORMATION: 10-88-81 : polymorph

US-09-641-638-880

Query match	0.98;	Score 22.
Best Local Similarity	66.78;	Pred. No.
Matches	30.	Conservation
	1.	Mismatches

3107 ATCTTTTTTATAATAATATATTTTCTAAAA
MATCHES 30; CONSERVATIVE 1; MISMA

Db 47 ATGTTTGATTGATTTCAACATAGRTTTTCCAGT

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RESULT 20
US-08-975-703-31
Sequence 31, Application US/08975703
Patent No. 6030832
GENERAL INFORMATION:
APPLICANT: Wong, Alexander K.C.
APPLICANT: Bartel, Paul L.
APPLICANT: Teng, David H.-F.
APPLICANT: Tavtigian, Sean V.
TITLE OF INVENTION: A Carboxy-Terminal BRCA1 Interacting
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Fig9, Ernst & Kurz, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701 East
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,703
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 2318-0174
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-624-1589
TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Primer"
US-08-975-703-31

Query Match 0.9%; Score 22; DB 3; Length 42;
Best Local Similarity 73.7%; Pred. No. 4.8e+03;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2034 TTTTCCAGGCAAAATGGAGGCAAGCAAGAAAGAA 2071
DB 2 TTTTCCAGTCAGCGGAGGAAATCACAAGAAACA 39

RESULT 21
US-09-515-884-31
Sequence 31, Application US/09515884
Patent No. 6235263
GENERAL INFORMATION:
APPLICANT: Wong, Alexander K.C.
APPLICANT: Bartel, Paul L.
APPLICANT: Teng, David H.-F.
APPLICANT: Tavtigian, Sean V.
TITLE OF INVENTION: A Carboxy-Terminal BRCA1 Interacting
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Fig9, Ernst & Kurz, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701 East
CITY: Washington
STATE: DC

COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/515,884
FILING DATE: 29-Feb-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,703
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 2318-0174
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-624-1589
TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Primer"
US-09-515-884-31

Query Match 0.9%; Score 22; DB 4; Length 42;
Best Local Similarity 73.7%; Pred. No. 4.8e+03;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2034 TTTTCCAGGCAAAATGGAGGCAAGCAAGAAAGAA 2071
DB 2 TTTTCCAGTCAGCGGAGGAAATCACAAGAAACA 39

RESULT 22
US-08-860-038-16/c
Sequence 16, Application US/08860038
Patent No. 6287762
GENERAL INFORMATION:
APPLICANT: CROUZET, Joel
APPLICANT: SCHERMAN, Daniel
TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION
TITLE OF INVENTION: WITH AN IMMOBILIZED OLIGONUCLEOTIDE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Atcoila Road, Mailstop 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,038
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/15162
FILING DATE: 16-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR95/01468

FILING DATE: 08-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky Esq., Martin F.
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: ST94090-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3816
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide"
US-08-860-038-16

Query Match 0.9%; Score 22; DB 4; Length 58;
Best Local Similarity 63.0%; Pred. No. 5.7e+03;
Matches 34; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 123 GGACGACCCGAGAGCGCGCTCTGAGATGAGCTGAGAGGGGGGTCAATT 176
DB 54 GGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGATT 1

RESULT 23
US-09-580-923-16/c
Sequence 16, Application US/09580923
Patent No. 6319672
GENERAL INFORMATION:
APPLICANT: Crouzet, Joel
APPLICANT: Scherman, Daniel
APPLICANT: Wills, Pierre
APPLICANT: Cameron, Beatrice
APPLICANT: Blanchet, Francis
TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN
TITLE OF INVENTION: IMMobilized OLIGONUCLEOTIDE
FILE REFERENCE: 03804.0138-01
CURRENT APPLICATION NUMBER: US/09/580,923
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 08/860,038
PRIOR FILING DATE: 1997-06-09
PRIOR APPLICATION NUMBER: PCT/FR95/01468
PRIOR FILING DATE: 1995-11-08
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 58
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
US-09-580-923-16

Query Match 0.9%; Score 22; DB 4; Length 58;
Best Local Similarity 63.0%; Pred. No. 5.7e+03;
Matches 34; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 123 GGACGACCCGAGAGCGCGCTCTGAGATGAGCTGAGAGGGGGGTCAATT 176
DB 54 GGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGATT 1

RESULT 24
US-09-021-560-5
Sequence 5, Application US/09021560
Patent No. 6410719
GENERAL INFORMATION:
APPLICANT: BOREN, THOMAS
APPLICANT: NORMARK, STAFFAN

APPLICANT: ARNOVIST, ANNA
APPLICANT: ILLER, DAG
TITLE OF INVENTION: BLOOD GROUP ANTIGEN BINDING PROTEIN AND
TITLE OF INVENTION: CORRESPONDING GENES
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/021,560
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 825-144P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-09-021-560-5

Query Match 0.9%; Score 22; DB 4; Length 60;
Best Local Similarity 63.0%; Pred. No. 5.8e+03;
Matches 34; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 49 GACGGCTTTTACCCAGCCCGACTTCGAGACGAGGAAGCTGAGACATGCA 102
DB 7 GACGGCTTTTACACACGTCGAGGCTATCAATGCTGAGAGCCGCTCAATGCTA 60

RESULT 25
US-08-983-607-7/c
Sequence 7, Application US/08983607
Patent No. 6140470
GENERAL INFORMATION:
APPLICANT: Alan Garen
APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Department of Molecular Biophysics
ADDRESSEE: and Biochemistry, Yale University
STREET: 266 Whitney Avenue
CITY: New Haven
STATE: Connecticut
COUNTRY: United States of America
ZIP: 06520-8114
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 MB diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,607
FILING DATE: April 27, 1998
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mary M. Krinsky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-679
TELEPHONE: 203-773-9544
TELEFAX: 203-773-1183
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 residues
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
DESCRIPTION: primer used in constructs
US-08-983-607-7

Query Match 0.9%; Score 21.8; DB 3; Length 50;
Best Local Similarity 67.4%; Pred. No. 5.9e+03;
Matches 29; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

Qy 1501 GCATCGGACCACTTCCATACGACAGCCGCACTCTGGGCCAT 1543
Db 43 SCAMCAGCTGACCTCGGCCACGTGCGCCGACCTTGAGCCAT 1

RESULT 26
US-08-983-607-44/c
Sequence 44, Application US/08983607
Patent No. 6140470
GENERAL INFORMATION:
APPLICANT: Alan Garen
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bcdies
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Department of Molecular Biophysics
ADDRESSER: and Biochemistry, Yale University
STREET: 266 Whitney Avenue
CITY: New Haven
STATE: Connecticut
COUNTRY: United States of America
ZIP: 06520-8114
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: word processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,607
FILING DATE: April 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mary M. Krinsky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-679
TELEPHONE: 203-773-9544
TELEFAX: 203-773-1183
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 residues
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA
DESCRIPTION: primer used in constructs
US-08-983-607-44

Query Match 0.9%; Score 21.8; DB 3; Length 50;
Best Local Similarity 67.4%; Pred. No. 5.9e+03;
Matches 29; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

Qy 1501 GCATCGGACCACTTCCATACGACAGCCGCACTCTGGGCCAT 1543
Db 43 SCAMCAGCTGACCTCGGCCACGTGCGCCGACCTTGAGCCAT 1

RESULT 27
US-08-821-559A-12
Sequence 12, Application US/08821559A
Patent No. 5846774
GENERAL INFORMATION:
APPLICANT: XIA, YUANNAN
TITLE OF INVENTION: CHLORELLA VIRUS PROMOTERS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSER: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 5846774west Center, 90 South Seventh St
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,559A
FILING DATE: 21-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 8648.63-US-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5268
TELEFAX: 612/332-9081
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-821-559A-12

Query Match 0.9%; Score 21.4; DB 2; Length 48;
Best Local Similarity 66.0%; Pred. No. 7.5e+03;
Matches 31; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 2233 CTTCTCTGTGTAATATATATGCAATGATTCATTTGTAACACA 2279
Db 2 CTTATCGTTGATGATGATTAATGACAAATGACGCTGATACACA 48

RESULT 28
US-09-400-541-12
Sequence 12, Application US/09400541
Patent No. 6316224
GENERAL INFORMATION:
APPLICANT: BIONEERASKA, INC.

APPLICANT: PICKUP, David J.
APPLICANT: PATEL, Dhaval Kumar
APPLICANT: ANTZAK, James B.
TITLE OF INVENTION: SITE-SPECIFIC RNA CLEAVAGE
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/113,646A
FILING DATE: 31-AUG-1993
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/084,406
FILING DATE: 10-AUG-1987
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-20
TELEPHONE: (703) 816-4000
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
US-08-113-646A-41

Query Match 0.9%; Score 21.4; DB 1; Length 55;
Best Local Similarity 57.4%; Pred. No. 8.1e+03;
Matches 27; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 1754 GATTTAAATCAATCATGTCGCAAAAAAAGCTTAAGCAAAA 1800
DB 8 GAUU 54

RESULT 32
US-08-143-219-18
Sequence 18, Application US/08143219
Patent No. 5670330
GENERAL INFORMATION:
APPLICANT: Sonnenberg, Nahum
APPLICANT: Katze, Michael G.
APPLICANT: Roy, Sophie
APPLICANT: Koromilas, Antonis E.
APPLICANT: Barber, Glen N.
TITLE OF INVENTION: TUMOR-CELL ASSAY METHOD AND KIT
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM compatible
OPERATING SYSTEM: PC-DOS (Version 5.0)

SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/143,219
FILING DATE: October 25, 1993
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/141,244
FILING DATE: October 22, 1993
APPLICATION NUMBER: 07/953,681
FILING DATE: September 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Douglas E. Olson
REGISTRATION NUMBER: 22,798
REFERENCE/DOCKET NUMBER: 204/139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: COMPLEMENTARY TO THE RNA PROBE FOR
INDIVIDUAL ISOLATE: PR-VI, FIGURE 5
US-08-143-219-18

Query Match 0.9%; Score 21.4; DB 1; Length 60;
Best Local Similarity 61.8%; Pred. No. 8.4e+03;
Matches 34; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 644 TGGGGCATTTACATCAAAAGGGATCATCTACAGAGCTGAAGCCGAGAAATAT 698
DB 5 TGGATATATATCATCAATCAAAAAAATATATCATAGAGATCTTAAGCCAAATATAT 59

RESULT 33
US-08-584-040-8235
Sequence 8235, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Payco, Pamela
APPLICANT: McSwigen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040

```

?      FILING DATE: January 11, 1996
?      CLASSIFICATION: 514
?      PRIOR APPLICATION DATA:
?      APPLICATION NUMBER: 60/005,974
?      FILING DATE: October 26, 1995
?      ATTORNEY/AGENT INFORMATION:
?      NAME: Macbush, Richard J.
?      REGISTRATION NUMBER: 32,327
?      REFERENCE/DOCKET NUMBER: 218,066
?      TELECOMMUNICATION INFORMATION:
?      TELEPHONE: (213) 489-1600
?      TELEFAX: (213) 955-0440
?      TELEX: 67-3510
?      INFORMATION FOR SEQ. ID NO.: 8235:
?      SEQUENCE CHARACTERISTICS:
?      LENGTH: 54 base pairs
?      TYPE: nucleic acid
?      STRANDEDNESS: single
?      TOPOLOGY: linear
?
US-08-584-040-8235

```

Query Match	0.9%;	Score	21.2;	DB	4;	Length	54;
Best Local Similarity	52.0%;	Pred.	No. 9e+03;				
Matches	26;	Conservative	6;	Mismatches	18;	Indels	0;
				Gaps			0

```

QY 2045 AAAATGGCAGGCCAAGACAAAGAACTTACCATTTGATGTTTACGTG 2094
      ||| : ||| ||| ||| ||| ||| : : ||| :
Db 2 AAUGUGAGAAGCCAAAGACCAGAGAAACACACGUGUGGACUUAACUG 51

```

```

RESULT 34
US-09-508-542-13
Sequence 13, Application US/09508542
Patent No. 6339174
GENERAL INFORMATION:
APPLICANT: STRAUSS, ANDREAS
APPLICANT: THUMM, GUNTHER
APPLICANT: POHLNER, JOHANNES
APPLICANT: GOTZ, FRIEDRICH
TITLE OF INVENTION: METHOD FOR IDENTIFYING A NUCLEIC ACID
FILE REFERENCE: 10496/P65266USO
CURRENT APPLICATION NUMBER: US/09/508,542
CURRENT FILING DATE: 2000-05-16
PRIORITY APPLICATION NUMBER: PCT/EP98/06136
PRIORITY FILING DATE: 1998-09-26
PRIORITY APPLICATION NUMBER: 97 116 841.4
PRIORITY FILING DATE: 1997-09-27
PRIORITY APPLICATION NUMBER: 97 118 755.4
PRIORITY FILING DATE: 1997-10-29
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 56
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-508-542-13

```

Query Match	0.9%	Score 21.2	DB 4	Length 56
Best Local Similarity	69.0%	Pred No. 9.2e+03		
Matches 29, Conservative	0	Mismatches 13	Indels 0	Gaps 0

```
QY      221 GCATGGAACATTGTGAGAAATTTGAAATCTCAGAAACTAGTG 262
          ||| | | | | | | | | | | | | | | | | | | |
Db       9 GCTTACCACAATCTAAGAATCTGAATATCTCAAGCAAGTG 50
```

RESULT 35
US-08-417-210A-103/C
; Sequence 103, Application US/08417210A
; Patent No. 5863542

```

1      GENERAL INFORMATION:
2      APPLICANT: PAOLETTI, ENZO
3      APPLICANT: TARTAGLIA, JAMES
4      APPLICANT: COX, WILLIAM I.
5      TITLE OF INVENTION: IMMUNODEFICIENCY RECOMBINANT POXVIRUS
6      NUMBER OF SEQUENCES: 148
7      CORRESPONDENCE ADDRESS:
8      ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
9      STREET: 530 FIFTH AVENUE
10     CITY: NEW YORK
11     STATE: NEW YORK
12     COUNTRY: USA
13     ZIP: 10036
14     COMPUTER READABLE FORM:
15     MEDIUM TYPE: Floppy disk
16     COMPUTER: IBM PC compatible
17     OPERATING SYSTEM: PC-DOS/MS-DOS
18     SOFTWARE: Patent in Release #1.0, Version #1.30
19     CURRENT APPLICATION DATA:
20     APPLICATION NUMBER: US/08/417,210A
21     FILING DATE: 05-Apr-1995
22     CLASSIFICATION: 435
23     ATTORNEY/AGENT INFORMATION:
24     NAME: KOWALSKI, THOMAS J.
25     REGISTRATION NUMBER: 32,147
26     REFERENCE/DOCKET NUMBER: 454310-2690
27     TELECOMMUNICATION INFORMATION:
28     TELEPHONE: 212-840-3333
29     INFORMATION FOR SEQ ID NO: 103:
30     SEQUENCE CHARACTERISTICS:
31     LENGTH: 58 base pairs
32     TYPE: nucleic acid
33     STRANDEDNESS: single
34     TOPOLOGY: linear
35     MOLECULE TYPE: DNA (genomic)
36     OS-08-417-210A-103

```

Query Match	0.9%	Score 21.2;	DB 2;	Length 58;
Best Local Similarity	64.0%	Pred. No. 9.4e+03;		
Matches 32; Conservative	0;	Mismatches 18;	Indels 0;	Gaps 0;

Qy 2221 CAACTTCTGTTCTTCTTGGTGAATAATAAATGCAAATGAATCATTT 2270
 Db 51 CTAGCTGCTTCTTCTGTAGTGCATTTATATTTGTAATTATATATTTT 2

RESULT 36
 US-08-417-210A-108
 Sequence 108, Application US/08417210A
 Patent No. 5863542
 GENERAL INFORMATION:
 APPLICANT: PAOLETTI, ENZO
 APPLICANT: TARRAGLIA, JAMES
 APPLICANT: COX, WILLIAM I.
 TITLE OF INVENTION: IMMUNODEFICIENCY RECOMBINANT POXVIRUS
 NUMBER OF SEQUENCES: 148
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
 STREET: 530 FIFTH AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/417,210A
 FILING DATE: 05-Apr-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER: US/08/417,210A
FILING DATE: 05-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: KOWALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454310-2690
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-840-3333
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-417-210A-108

Query Match 0.9%; Score 21; DB 4; Length 58;
Best Local Similarity 64.0%; Pred. No. 9.4e+03;
Matches 32; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 2221 CAACTCTGTTCTCTCTGGAATTAATGAATGCAATGATCATT 2270
DB 7 CTAGCTCTGCTTCTCTGTTAGTGGCATTTATATTGTAATATATATT 56

RESULT 37
US-09-532-656-17
Sequence 17, Application US/09532656
Patent No. 6316608
GENERAL INFORMATION:
APPLICANT: Reynolds, Mark A.
APPLICANT: Ruvolo, Michael
APPLICANT: Arnold, Jr., Lyle J.
TITLE OF INVENTION: COMBINED POLYNUCLEOTIDE SEQUENCES AS DISCRETE ASSAY ENDPOINTS
FILE REFERENCE: IN-0017 US
CURRENT APPLICATION NUMBER: US/09/532,656
CURRENT FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PERL Program
SEQ ID NO 17
LENGTH: 59
TYPE: DNA
ORGANISM: Candida albicans
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6316608 F23S805
US-09-532-656-17

Query Match 0.9%; Score 21; DB 4; Length 59;
Best Local Similarity 66.7%; Pred. No. 1.1e+04;
Matches 30; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1078 TTCTTAGACACATTACTGGAAGAACTTCTGCTCGAAGGTG 1122
DB 5 TTCATTAGTGCATTTAAAGAGAAAGAACTGTTTGAATGTG 49

RESULT 38
US-09-775-319-4
Sequence 4, Application US/09775319
Patent No. 6387631
GENERAL INFORMATION:
APPLICANT: Arnold, Jr., Lyle J.
APPLICANT: Sawan, Samuel P.
APPLICANT: Lee, Paul H.
TITLE OF INVENTION: POLYMER COATED SURFACES FOR MICROARRAY APPLICATIONS
FILE REFERENCE: IN-0038 US
CURRENT APPLICATION NUMBER: US/09/775,319
CURRENT FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: 09/532,419
PRIOR FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PERL Program
SEQ ID NO 4
LENGTH: 59

TYPE: DNA
ORGANISM: Candida albicans
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6387631 F23S805
US-09-775-319-4

Query Match 0.9%; Score 21; DB 4; Length 59;
Best Local Similarity 66.7%; Pred. No. 1.1e+04;
Matches 30; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1078 TTCTTAGACACATTACTGGAAGAACTTCTGCTCGAAGGTG 1122
DB 5 TTCATTAGTGCATTTAAAGAGAAAGAACTGTTTGAATGTG 49

RESULT 39
US-09-532-419A-4
Sequence 4, Application US/09532419A
Patent No. 6413722
GENERAL INFORMATION:
APPLICANT: Arnold, Jr., Lyle J.
APPLICANT: Sawan, Samuel P.
APPLICANT: Lee, Paul H.
TITLE OF INVENTION: POLYMER COATED SURFACES FOR MICROARRAY APPLICATIONS
FILE REFERENCE: IN-0038 US
CURRENT APPLICATION NUMBER: US/09/532,419A
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PERL Program
SEQ ID NO 4
LENGTH: 59
TYPE: DNA
ORGANISM: Candida albicans
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6413722 F23S805
US-09-532-419A-4

Query Match 0.9%; Score 21; DB 4; Length 59;
Best Local Similarity 66.7%; Pred. No. 1.1e+04;
Matches 30; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1078 TTCTTAGACACATTACTGGAAGAACTTCTGCTCGAAGGTG 1122
DB 5 TTCATTAGTGCATTTAAAGAGAAAGAACTGTTTGAATGTG 49

RESULT 40
US-08-475-081-2
Sequence 2, Application US/08475081
Patent No. 5948894
GENERAL INFORMATION:
APPLICANT: Berry, Mark J.
APPLICANT: Davis, Paul J.
APPLICANT: Verhoeven, Martine E.
APPLICANT: De Winter, Ronald F.J.
TITLE OF INVENTION: REAGENTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: CUSHMAN, DARBY & CUSHMAN
STREET: Eleventh Floor, 1615 L. Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,081

FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/979,448
FILING DATE: 20-NOV-1992
APPLICATION NUMBER: US/07/628,910
FILING DATE: 18-DEC-1990
APPLICATION NUMBER: GB 8928501.9
FILING DATE: 18-DEC-1990
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 248453 CUSH
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: misc difference
LOCATION: replace(37..42, "")
OTHER INFORMATION: /note="nm nm represents (GCT
OTHER INFORMATION: ACC)n where n=0 to 5"
US-08-475-081-2

Query Match 0.9%; Score 21; DB 2; Length 60;
Best Local Similarity 62.8%; Pred. No. 1.1e+04;
Matches 27; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 58 TACCACAGCCCGGAGCTTCCGAGACGAGGAGGAGCATGG 100
DB 17 TACCCCTTACCGGATTCNNNNNNNGATCCTGAGGAGACGG 59

RESULT 41
US-09-641-638-1114
Sequence 1114, Application US/09641638
Patent No. 6432648
GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIOMOLECULAR MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GENSET.051CPI
CURRENT APPLICATION NUMBER: US/09/641,638
PRIOR FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent.pm
SEQ ID NO 1114
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 12-316-292 : polymorphic base C or T
NAME/KEY: misc_feature
LOCATION: 47
OTHER INFORMATION: n=a, g, c or t
US-09-641-638-1114

Query Match 0.9%; Score 20.6; DB 4; Length 47;

Best Local Similarity 67.4%; Pred. No. 1.2e+04;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 850 GATTGGTGAGTGTGGAGCATTAATGTATGATGCTGACTG 892
DB 4 GAATGGTCTCTCTGGGTGCTGATTTCTTACATGATGCTG 46

RESULT 42
US-08-860-038-17
Sequence 17, Application US/08860038
Patent No. 6287762
GENERAL INFORMATION:
APPLICANT: CROUZET, Joel
APPLICANT: SCHERMAN, Daniel
APPLICANT: WILS, Pierre
TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION
TITLE OF INVENTION: WITH AN IMMOBILIZED OLIGONUCLEOTIDE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESS: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,038
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/15162
FILING DATE: 16-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR95/01468
FILING DATE: 08-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky Esq., Martin F.
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: ST94090-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3816
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide"
US-08-860-038-17

Query Match 0.9%; Score 20.6; DB 4; Length 50;
Best Local Similarity 67.4%; Pred. No. 1.3e+04;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 132 AGAGGAGCGGGGCTGTGAGGATGAGCTGAGGAGGAGGAGG 174
DB 3 AGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 45

RESULT 43
US-09-580-923-117
Sequence 17, Application US/09580923
Patent No. 6319672
GENERAL INFORMATION:
APPLICANT: Crouzet, Joel

APPLICANT: Scherman, Daniel
APPLICANT: Wils, Pierre
APPLICANT: Cameron, Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN
TITLE OF INVENTION: IMMOBILIZED OLIGONUCLEOTIDE
FILE REFERENCE: 03804.0138-01
CURRENT APPLICATION NUMBER: US/09/580,923
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 08/860,038
PRIOR FILING DATE: 1997-06-09
PRIOR APPLICATION NUMBER: PCT/FR95/01468
PRIOR FILING DATE: 1995-11-08
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
US-09-580-923-17

Query Match 0.9%; Score 20.6; DB 4; Length 50;
Best Local Similarity 67.4%; Pred. No. 1.3e+04;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 132 AGAGACCGGGCTCTGAGATGAGCTGGAGAGGGGGGTAG 174
DB 3 AG 45

RESULT 44
US-08-929-501-24
Sequence 24, Application US/08929501
Patent No. 5854051
GENERAL INFORMATION:
APPLICANT: Ramaswamy Chandrashekar
APPLICANT: Naotoshi Tsuji
TITLE OF INVENTION: PARASITIC HELMINTH ASPARAGINASE
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, AND
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/929,501
FILING DATE: 15-SEP-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: Primer
US-08-929-501-24

Query Match 0.9%; Score 20.6; DB 2; Length 51;
Best Local Similarity 67.4%; Pred. No. 1.3e+04;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1848 CATCTTCTCACTTATCAAGATTTTCATGTGACTCG 1890
DB 9 CTCTTACTGAACTTTTTCATCTTTTCATCTAATGACTAG 51

RESULT 45
US-09-140-177-24
Sequence 24, Application US/09140177
Patent No. 6042825
GENERAL INFORMATION:
APPLICANT: Ramaswamy Chandrashekar
APPLICANT: Naotoshi Tsuji
TITLE OF INVENTION: PARASITIC HELMINTH ASPARAGINASE
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, AND
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/140,177
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: 08/929,501
APPLICATION NUMBER: 08/929,501
FILING DATE: 15-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Primer
US-09-140-177-24

Query Match 0.9%; Score 20.6; DB 3; Length 51;
Best Local Similarity 67.4%; Pred. No. 1.3e+04;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1848 CATCTTCTCACTTATCAAGATTTTCATGTGACTCG 1890
DB 9 CTCTTACTGAACTTTTTCATCTTTTCATCTAATGACTAG 51

RESULT 46
US-09-397-979-24
Sequence 24, Application US/09397979
Patent No. 6165735

GENERAL INFORMATION:
APPLICANT: Ramaswamy Chandrashekar
TITLE OF INVENTION: PARASITIC HELMINTH ASPARAGINASE
TITLE OF INVENTION: PROTEIN, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/397,979
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/929,501
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HM-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Primer
US-09-397-979-24

Query Match 0.9%; Score 20.6; DB 4; Length 51;
Best Local Similarity 67.4%; Pred. No. 1.3e+04;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1848 CATCTTTCACCTTATCAAGATTTCATGTTGATGACTCG 1890
DB 9 CTCTTACTGAACTTTTCATCTTTTCATTTCAATGACTAG 51

RESULT 47
US-08-171-389-19
Sequence 19, Application US/08171389
Patent No. 5578444
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,389
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human alcohol dehydrogenase beta
INDIVIDUAL ISOLATE: subunit gene
US-08-171-389-19

Query Match 0.9%; Score 20.2; DB 1; Length 48;
Best Local Similarity 68.3%; Pred. No. 1.6e+04;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2082 GATGTTTACGTCGAACCAACCGATCTTTTATATATA 2122
DB 1 GATGTTACCAAGCAACAAATAATATCTGTCAATATA 41

RESULT 48
US-08-123-936-19
Sequence 19, Application US/08123936
Patent No. 5726014
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
TITLE OF INVENTION: Screening Assay for the Detection of
TITLE OF INVENTION: DNA-Binding Molecules
NUMBER OF SEQUENCES: 640
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,936
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fadian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0075.32/G19P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human alcohol dehydrogenase beta
INDIVIDUAL ISOLATE: subunit gene
US-08-123-936-19

Query Match 0.9%; Score 20.2; DB 1; Length 48;
Best Local Similarity 68.3%; Pred. No. 1.6e+04;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2082 GATGTTTACGTGCAACACCTGGAATCTTTTATATA 2122
Db 1 GATGTTACACAGCAACAAATAATATCTGTGCAATATA 41

RESULT 49
US-08-475-228A-19
Sequence 19, Application US/08475228A
Patent No. 5869241
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: GeneLabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,228A
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 4600-0175.21/G19P3D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human alcohol dehydrogenase beta
INDIVIDUAL ISOLATE: subunit gene
US-08-475-228A-19

Query Match 0.9%; Score 20.2; DB 2; Length 48;
Best Local Similarity 68.3%; Pred. No. 1.6e+04;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2082 GATGTTTACGTGCAACACCTGGAATCTTTTATATA 2122
Db 1 GATGTTACACAGCAACAAATAATATCTGTGCAATATA 41

RESULT 50
US-08-482-080A-19
Sequence 19, Application US/08482080A
Patent No. 6010849
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: GeneLabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,080A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/171,389
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992

APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Brady, John F.
REGISTRATION NUMBER: 39,118
REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human alcohol dehydrogenase beta
US-08-482-080A-19

Query Match 0.9%; Score 20.2; DB 3; Length 48;
Best Local Similarity 68.3%; Pred. No. 1.6e+04;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 2082 GATGTTTACGTGCAACAACTGAATCTTTTATATA 2122
Db 1 GATGTTACACAGCAACAAATAATATCTGTGCATATA 41

RESULT 51
US-09-354-947-19
Sequence 19, Application US/09354947
Patent No. 6384208
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/354,947
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,080
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/171,389
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992

APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Brady, John F.
REGISTRATION NUMBER: 39,118
REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human alcohol dehydrogenase beta
US-09-354-947-19

Query Match 0.9%; Score 20.2; DB 4; Length 48;
Best Local Similarity 68.3%; Pred. No. 1.6e+04;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 2082 GATGTTTACGTGCAACAACTGAATCTTTTATATA 2122
Db 1 GATGTTACACAGCAACAAATAATATCTGTGCATATA 41

RESULT 52
PCT-US93-12388-19
Sequence 19, Application PC/TUS9312388
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12388
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175.41/G19PCT2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human alcohol dehydrogenase beta
PCT-US93-12386-19

Query Match 0.9%; Score 20.2; DB 5; Length 48;
Best Local Similarity 68.3%; Pred. No. 1.6e+04;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2082 GATGTTTACGTCGAACCACTGATTTTATATA 2122
DB 1 GATGTTACACAGCAACAAATAATATCTGTCAATATA 41

RESULT 53
US-08-171-382-11/c
Sequence 11, Application US/08171382
Patent No. 5472856
GENERAL INFORMATION:
APPLICANT: Harris, Crafford A.
APPLICANT: Goldstein, Gideon
APPLICANT: Siekierka, John J.
APPLICANT: Talle, Mary Anne
APPLICANT: Shenbagamurthi, Ponniah
APPLICANT: Culler, Michael D.
APPLICANT: Secavage, Diane R.
TITLE OF INVENTION: Recombinant Human Thymoplectin Proteins
TITLE OF INVENTION: and Uses Therefor
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: Howson and Howson
STREET: Spring House Corporate Cntr, P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,382
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: IRI43USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5618
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
US-08-171-382-11

Query Match 0.9%; Score 20.2; DB 1; Length 50;
Best Local Similarity 68.3%; Pred. No. 1.6e+04;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2226 TCTGTTCTCTCTTGTGGAATAATAAATGCAATGAAAT 2266

DB 42 TCTAATCTCTCATGTTGACCTAGAAAATCCAACTGAAT 2

RESULT 54
US-08-584-760A-33/c
Sequence 33, Application US/08584760A
Patent No. 6290953
GENERAL INFORMATION:
APPLICANT: Ballance, David J
APPLICANT: Courtney, Michael G
APPLICANT: Fimmis, Christopher J A
APPLICANT: Sleep, Darrell
TITLE OF INVENTION: Medicine
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSER: Centeon L.L.C.
STREET: 1020 First Avenue
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-1310
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,760A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/211,860
FILING DATE: 15-APR-1994
APPLICATION NUMBER: GB 9121815.6
FILING DATE: 14-OCT-1891
ATTORNEY/AGENT INFORMATION:
NAME: Naomi Biswas
REGISTRATION NUMBER: 38,384
REFERENCE/DOCKET NUMBER: 92H853-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610/878-4294
TELEFAX: 610/878/4221
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..60
OTHER INFORMATION: /function="oligonucleotide 32"
US-08-584-760A-33

Query Match 0.9%; Score 20.2; DB 4; Length 60;
Best Local Similarity 63.3%; Pred. No. 1.8e+04;
Matches 31; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 378 GAAATATTTGCCATGAGGTGCTTAAAGCAATGATAGTAAAT 426
DB 58 GAAACACTGCGAAGAGCTGCTTAAAGCTGTAAAGCTCTATTAAAT 10

RESULT 55
US-08-222-177A-349
Sequence 349, Application US/08222177A
Patent No. 5582979
GENERAL INFORMATION:
APPLICANT: Weber, James L.

TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dc-da)n (dg-dt)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
ADDRESSEE: Demitt Ross & Stevens, S.C.
STREET: 8000 Excelator Drive, Suite 401
CITY: Madison
STATE: Wisconsin
COUNTRY: USA
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/222,177A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-Apr-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
TELEX:
INFORMATION FOR SEQ ID NO: 349:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: mfd10rs
US-08-222-177A-349

Query Match 0.9%; Score 20; DB 1; Length 46;
Best Local Similarity 65.9%; Pred. No. 1.8e+04;
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 2111 TTTTATTAATAATATATTTTCAATGATTTGATCA 2154
DB 2 TTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 45

RESULT 56
US-09-338-907-315
Sequence 315, Application US/09338907
Patent No. 6265546
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marla
APPLICANT: Ilya, Chumakov
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: PROSTATE CANCER GENE
FILE REFERENCE: GENSET.18C1CP
CURRENT APPLICATION NUMBER: US/09/338,907
CURRENT FILING DATE: 1999-06-23
EARLIER APPLICATION NUMBER: 08/996,306
EARLIER FILING DATE: 1997-12-22
EARLIER APPLICATION NUMBER: 60/099,658
EARLIER FILING DATE: 1998-09-09
EARLIER APPLICATION NUMBER: 09/218,207
EARLIER FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 578
SOFTWARE: Patent.pm
SEQ ID NO 315
LENGTH: 47

TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 1..47
OTHER INFORMATION: polymorphic fragment 99-147-181, variant version of SEQ ID238
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: base G ; A in SEQ ID238
FEATURE:
NAME/KEY: primer_bind
LOCATION: 1..23
OTHER INFORMATION: potential microsequencing oligo 99-147-181.mis1
FEATURE:
NAME/KEY: primer_bind
LOCATION: 25..47
OTHER INFORMATION: complement potential microsequencing oligo 99-147-181.mis2
US-09-218-207-315

Query Match 0.9%; Score 20; DB 4; Length 47;
Best Local Similarity 72.2%; Pred. No. 1.8e+04;
Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 397 GTGCTTAAAAAGCAATGATAGTAAATGCTAAA 432
DB 3 GTCATGAAAAAGCATGATGAGAAAGAAACTTAA 38

RESULT 57
US-09-218-207-315
Sequence 315, Application US/09218207
Patent No. 6346381
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marla
APPLICANT: Ilya, Chumakov
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Prostate cancer gene
FILE REFERENCE: GENSET.018C1P
CURRENT APPLICATION NUMBER: US/09/218,207
CURRENT FILING DATE: 1998-12-22
EARLIER APPLICATION NUMBER: 08/996,306
EARLIER FILING DATE: 1997-12-22
EARLIER APPLICATION NUMBER: 60/099,658
EARLIER FILING DATE: 1998-09-09
NUMBER OF SEQ ID NOS: 578
SOFTWARE: Patent.pm
SEQ ID NO 315
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 1..47
OTHER INFORMATION: polymorphic fragment 99-147-181, variant version of SEQ ID238
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: base G ; A in SEQ ID238
FEATURE:
NAME/KEY: primer_bind
LOCATION: 1..23
OTHER INFORMATION: potential microsequencing oligo 99-147-181.mis1
FEATURE:
NAME/KEY: primer_bind
LOCATION: 25..47
OTHER INFORMATION: complement potential microsequencing oligo 99-147-181.mis2
US-09-218-207-315

Query Match 0.9%; Score 20; DB 4; Length 47;
Best Local Similarity 72.2%; Pred. No. 1.8e+04;
Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,101
FILING DATE: 01-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2740
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-458-101-102

Query Match 0.9%; Score 20; DB 1; Length 49;
Best Local Similarity 65.9%; Pred. No. 1.8e+04;
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 2109 CTTTATTTTATTAATATATATTTTCAATAGATTGTTGATT 2152
DB 45 CATTATATGTTATATATATTTTCAATTTGAGATCGAAT 2

RESULT 61
US-09-457-959-8
Sequence 8, Application US/09457959
Patent No. 6362002
GENERAL INFORMATION:
APPLICANT: Denison, Timothy J. et al.
TITLE OF INVENTION: Characterization of Individual Polymer
FILE REFERENCE: 00246/522001
CURRENT APPLICATION NUMBER: US/09/457,955
CURRENT FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: US-09/098,142
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: US 08/405,735
PRIOR FILING DATE: 1995-03-17
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 60
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-457-959-8

Query Match 0.9%; Score 20; DB 4; Length 60;
Best Local Similarity 58.3%; Pred. No. 2e+04;
Matches 35; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1741 AAAAATTAACGTGATTTTAAAAATCAATGTCAGAAAAAAGCAAAA 1800
DB 1 AA 60

RESULT 62
US-08-750-128-8
Sequence 8, Application US/08750128
Patent No. 5916773
GENERAL INFORMATION:
APPLICANT: MELE Antonio,
APPLICANT: DE SANTIS Rita,
APPLICANT: CARLOTTI Cristina,
APPLICANT: COSCARIELLA Annamaria

TITLE OF INVENTION: Hybrid molecule of formula GM-CSF-L-EPO or
TITLE OF INVENTION: EPO-L-GM-CSF for hematopoietic stimulation
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSER: LOWE, PRICE, LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 3.50 inch.
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,128
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT F1 94 A 000106
FILING DATE: 27-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Robert L. Price
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 2879-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
US-08-750-128-8

Query Match 0.8%; Score 19.8; DB 2; Length 48;
Best Local Similarity 63.8%; Pred. No. 2.1e+04;
Matches 30; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 127 CAGCGAGAGAGCGGCGCTCTGAGATGAGCTGAGAGAGCGGCTCA 173
DB 2 CCGCGGAGAGAGGCTCGGAGAGAGGCTTCGAGAGAGCGGCTCA 48

RESULT 63
US-09-461-697-233
Sequence 233, Application US/09461697
Patent No. 6277974
GENERAL INFORMATION:
APPLICANT: COGENET NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Putnam, Kasturi
TITLE OF INVENTION: KATZ, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 233
LENGTH: 48
TYPE: DNA
ORGANISM: Homo sapiens
US-09-461-697-233

Query Match 0.8%; Score 19.8; DB 4; Length 48;
Best Local Similarity 63.8%; Pred. No. 2.1e+04;
Matches 30; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1642 TGAAGAGGAGATGTGAGCATCTTGCAGAGTGAACAGACTCAA 1688
DB 2 TGAAGGTGGAATGAGAGAGAACTGGAAGAAAGAGAAAGATTAA 48

RESULT 64

US-08-105-483-103
Sequence 103, Application US/08105483
Patent No. 5494807

GENERAL INFORMATION:

APPLICANT: Paoletti, Enzo

TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE

TITLE OF INVENTION: STRAIN

NUMBER OF SEQUENCES: 462

CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis, Morris & Safford

STREET: 530 Fifth Avenue

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/105,483

FILING DATE: 12-AUG-1993

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/847,951

FILING DATE: 06-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: Frommer, William S.

REGISTRATION NUMBER: 25,506

REFERENCE/DOCKET NUMBER: 454310-2400

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 840-3333

TELEFAX: (212) 840-0712

INFORMATION FOR SEQ ID NO: 103:

SEQUENCE CHARACTERISTICS:

LENGTH: 49 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-105-483-103

Query Match 0.8%; Score 19.8; DB 1; Length 49;
Best Local Similarity 63.8%; Pred. No. 2.1e+04;
Matches 30; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 2103 CTGAATCTTTTATATATATATATATATATTTTCAATAGATTG 2149
DB 3 CTCGCCATTTTATATGATATATATATATTTTCAATTTTGAGATCG 49

RESULT 65

US-08-709-209-103
Sequence 103, Application US/08709209
Patent No. 5762938

GENERAL INFORMATION:

APPLICANT: Paoletti, Enzo

TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE

TITLE OF INVENTION: STRAIN

NUMBER OF SEQUENCES: 462

CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis, Morris & Safford

STREET: 530 Fifth Avenue

CITY: New York

STATE: NY

COUNTRY: USA

ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/709,209

FILING DATE: 21-AUG-1996

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/105,483

FILING DATE: 12-AUG-1993

APPLICATION NUMBER: US 07/847,951

FILING DATE: 06-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: Frommer, William S.

REGISTRATION NUMBER: 25,506

REFERENCE/DOCKET NUMBER: 454310-2400

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 840-3333

TELEFAX: (212) 840-0712

INFORMATION FOR SEQ ID NO: 103:

SEQUENCE CHARACTERISTICS:

LENGTH: 49 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-709-209-103

Query Match 0.8%; Score 19.8; DB 1; Length 49;
Best Local Similarity 63.8%; Pred. No. 2.1e+04;
Matches 30; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 2103 CTGAATCTTTTATATATATATATATATATTTTCAATAGATTG 2149
DB 3 CTCGCCATTTTATATGATATATATATATTTTCAATTTTGAGATCG 49

RESULT 66

US-08-458-101-103
Sequence 103, Application US/08458101
Patent No. 5766599

GENERAL INFORMATION:

APPLICANT: Paoletti, Enzo

APPLICANT: Perkins, Marion E.

APPLICANT: Taylor, Jill

APPLICANT: Tartaglia, James

APPLICANT: No. 5766599on, Elizabeth K.

APPLICANT: Riviere, Michel

APPLICANT: de Taisne, Charles

APPLICANT: Limbach, Keith J.

APPLICANT: Johnson, Gerard P.

APPLICANT: Pincus, Steven E.

APPLICANT: Cox, William I.

APPLICANT: Audinet, Jean-Christophe Francis

APPLICANT: Gettig, Russell Robert

TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE

TITLE OF INVENTION: STRAIN

NUMBER OF SEQUENCES: 467

CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis, Morris & Safford

STREET: 530 Fifth Avenue

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,101
FILING DATE: 01-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2740
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-458-101-103

Query Match 0.8%; Score 19.8; DB 1; Length 49;
Best Local Similarity 63.8%; Pred. No. 2.1e+04;
Matches 30; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 2103 CTGACCTCTTTTATTAATAATATATATTTTCAATAGATTTTGG 2149
Db 3 CTGCCCATTTTATTTGTATATATATATATTTTCAATTTTGAGATCTG 49

RESULT 67
US-09-423-744A-13/C
Sequence 13, Application US/09423744A
Patent No. 6372500
GENERAL INFORMATION:
APPLICANT: HSC Research and Development Limited Partnership
TITLE OF INVENTION: Episomal Expression Cassettes for Gene Therapy
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Rocky, Milnamov & Katz, Ltd.
STREET: 180 N. Stetson Avenue, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,744A
FILING DATE: 12-NO. 6372500-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA98/00478
FILING DATE: May 14, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
REFERENCE/DOCKET NUMBER: DWM6064P0020US
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: -

LOCATION: 1..54
IDENTIFICATION METHOD:
OTHER INFORMATION: /note="K183/SS synthetic DNA
oligo-nucleotide - amplification primer for PCR mutagenesis"
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-423-744A-13

Query Match 0.8%; Score 19.8; DB 4; Length 54;
Best Local Similarity 69.2%; Pred. No. 2.2e+04;
Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2097 AACACCTGAATCTTTTATTAATAATATATTTT 2135
Db 48 AACACCTCTCTTTTATTTTTCAGTCTGTTTAT 10

RESULT 68
US-09-415-784-11/C
Sequence 11, Application US/09415784
Patent No. 6391632
GENERAL INFORMATION:
APPLICANT: Dubensky Jr., Thomas W.
Polo, John M.
Belli, Barbara A.
Schlesinger, Sondra
Dryga, Sergey A.
Frolov, Ilva
TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
SYNTHESIS
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/415,784
FILING DATE: 08-Oct-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.457D1 /1196.006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-415-784-11

Query Match 0.8%; Score 19.8; DB 4; Length 58;
Best Local Similarity 63.8%; Pred. No. 2.3e+04;
Matches 30; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1743 AATTAAGTGAATTTTAAATAATCAATGATGCAAAAAAAC 1789
Db 57 AACAAAAATTTGTTTAACTTCAAAAAATTTTTTTTTTAAAC 11

RESULT 69

US-09-415-785A-11/C
Sequence 11, Application US/09415785A
Patent No. 6426196
GENERAL INFORMATION:
APPLICANT: Dubensky Jr., Thomas W.
Polo, John M.
Bell, Barbara A.
Schlesinger, Sondra
Dryga, Sergey A.
Frolov, Ilya
TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
SYNTHESIS
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/415,785A
FILING DATE: 08-Oct-1999
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.457D1 /1196.006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-415-785A-11
Query Match 0.8%; Score 19.8; DB 4; Length 58;
Best Local Similarity 63.8%; Pred. No. 2.3e+04;
Matches 30; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 1743 AATTAACGTGATTTTAAATCAATCATGTCACAAAAAAC 1789
DB 57 AACAAATTTGTTTAACTTTCACAAAAAACAAAAAAC 11
RESULT 70
US-08-944-465-11/C
Sequence 11, Application US/08944465
Patent No. 6451592
GENERAL INFORMATION:
APPLICANT: Dubensky Jr., Thomas W.
Polo, John M.
Bell, Barbara A.
Schlesinger, Sondra
Dryga, Sergey A.
Frolov, Ilya
TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
SYNTHESIS
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Avenue, Suite 6300

CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,465
FILING DATE: 06-Oct-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.457C4 / 1196.005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-944-465-11
Query Match 0.8%; Score 19.8; DB 4; Length 58;
Best Local Similarity 63.8%; Pred. No. 2.3e+04;
Matches 30; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 1743 AATTAACGTGATTTTAAATCAATCATGTCACAAAAAAC 1789
DB 57 AACAAATTTGTTTAACTTTCACAAAAAACAAAAAAC 11
RESULT 71
US-09-415-868-11/C
Sequence 11, Application US/09415868
Patent No. 6458560
GENERAL INFORMATION:
APPLICANT: Dubensky Jr., Thomas W.
Polo, John M.
Bell, Barbara A.
Schlesinger, Sondra
Dryga, Sergey A.
Frolov, Ilya
TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
SYNTHESIS
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/415,868
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/944,465
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.

REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.457C4 / 1196.005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-415-868-11

Query Match 0.8%; Score 19.8; DB 4; Length 58;
Best Local Similarity 63.8%; Pred. No. 2.3e+04;
Matches 30; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 1743 AATAAAGTGATTTTAAATAATCAATGTCGCAAAAAAAC 1789
Db 57 AACAAATTTGTTTAAACATTTCAAAAAAATTTTAAAC 11

RESULT 72
US-09-415-900-11/c
Sequence 11, Application US/09415900
Patent No. 6465634.
GENERAL INFORMATION:
APPLICANT: Dubensky Jr., Thomas W.
APPLICANT: Folo, John W.
APPLICANT: Belli, Barbara A.
APPLICANT: Schlesinger, Sondra
APPLICANT: Dryga, Sergey A.
APPLICANT: Frolow, Ilya
TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
TITLE OF INVENTION: WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
NUMBER OF SEQUENCES: 125
SYNTHESIS
CORRESPONDENCE ADDRESSES:
ADDRESSER: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/415,900
FILING DATE: 08-Oct-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMaster, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.457D4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-415-900-11

Query Match 0.8%; Score 19.8; DB 4; Length 58;
Best Local Similarity 63.8%; Pred. No. 2.3e+04;
Matches 30; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
Qy 1743 AATAAAGTGATTTTAAATAATCAATGTCGCAAAAAAAC 1789

Db 57 AACAAATTTGTTTAAACATTTCAAAAAAATTTTAAAC 11

RESULT 73
US-08-350-260A-250/c
Sequence 250, Application US/08350260A
Patent No. 5962255
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Nieslin, Ahuva
APPLICANT: Johnson, Kevin Stuart
APPLICANT: Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
TITLE OF INVENTION: binding pairs
NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESSES:
ADDRESSER: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01134
FILING DATE: 10-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 250:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-350-260A-250

Query Match 0.8%; Score 19.6; DB 2; Length 48;
Best Local Similarity 63.6%; Pred. No. 2.3e+04;

ORIGINAL SOURCE:
US-08-508-088-1

Query Match 0.8%; Score 19.6; DB 2; Length 60;
Best Local Similarity 62.0%; Pred. No. 2.6e+04;
Matches 31; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 5 GAGGCTGCGGCGGCTCCGCGCCATGAGCGACGAGAGGCGGACGCGC 54
DB 2 GCGGCGGCGGCTCCGCGCCATGAGCGACGAGAGGCGGACGCGC 51

RESULT 77

US-09-009-925-1
Sequence 1, Application US/0909925
Patent No. 5998208

GENERAL INFORMATION:

APPLICANT: CHILDREN'S MEDICAL CENTER CORPORATION
TITLE OF INVENTION: HELPER VIRUS-FREE HERPESVIRUS VECTOR PACKAGING SYSTEM
NUMBER OF SEQUENCES: 6
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSER: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,925
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12033
FILING DATE: 22-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/508,088
FILING DATE: 26-JUL-1995

ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45485-CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:

US-09-009-925-1

Query Match 0.8%; Score 19.6; DB 2; Length 60;
Best Local Similarity 62.0%; Pred. No. 2.6e+04;
Matches 31; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 5 GAGGCTGCGGCGGCTCCGCGCCATGAGCGACGAGAGGCGGACGCGC 54
DB 2 GCGGCGGCGGCTCCGCGCCATGAGCGACGAGAGGCGGACGCGC 51

RESULT 78

US-08-068-747-9/c

Query Match 0.8%; Score 19.6; DB 2; Length 60;
Best Local Similarity 62.0%; Pred. No. 2.6e+04;
Matches 31; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 5 GAGGCTGCGGCGGCTCCGCGCCATGAGCGACGAGAGGCGGACGCGC 54
DB 2 GCGGCGGCGGCTCCGCGCCATGAGCGACGAGAGGCGGACGCGC 51

RESULT 79

US-08-068-747-9/c

Query Match 0.8%; Score 19.6; DB 2; Length 60;
Best Local Similarity 62.0%; Pred. No. 2.6e+04;
Matches 31; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 5 GAGGCTGCGGCGGCTCCGCGCCATGAGCGACGAGAGGCGGACGCGC 54
DB 2 GCGGCGGCGGCTCCGCGCCATGAGCGACGAGAGGCGGACGCGC 51

RESULT 78

US-08-068-747-9/c

Query Match 0.8%; Score 19.6; DB 2; Length 60;
Best Local Similarity 62.0%; Pred. No. 2.6e+04;
Matches 31; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 5 GAGGCTGCGGCGGCTCCGCGCCATGAGCGACGAGAGGCGGACGCGC 54
DB 2 GCGGCGGCGGCTCCGCGCCATGAGCGACGAGAGGCGGACGCGC 51

RESULT 79

US-08-068-747-9/c

Query Match 0.8%; Score 19.6; DB 2; Length 60;
Best Local Similarity 62.0%; Pred. No. 2.6e+04;
Matches 31; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 5 GAGGCTGCGGCGGCTCCGCGCCATGAGCGACGAGAGGCGGACGCGC 54
DB 2 GCGGCGGCGGCTCCGCGCCATGAGCGACGAGAGGCGGACGCGC 51

RESULT 78

US-08-068-747-9/c

Query Match 0.8%; Score 19.6; DB 2; Length 60;
Best Local Similarity 62.0%; Pred. No. 2.6e+04;
Matches 31; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 5 GAGGCTGCGGCGGCTCCGCGCCATGAGCGACGAGAGGCGGACGCGC 54
DB 2 GCGGCGGCGGCTCCGCGCCATGAGCGACGAGAGGCGGACGCGC 51

RESULT 79

Sequence 9, Application US/08068747
Patent No. 5695933

GENERAL INFORMATION:
APPLICANT: Schalling, Martin
APPLICANT: Hudson, Thomas J.
APPLICANT: Housman, David E.

TITLE OF INVENTION: Direct Determination of Expanded
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/068,747
FILING DATE: 28-MAY-1993
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-6141
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic"

US-08-068-747-9

Query Match 0.8%; Score 19.4; DB 1; Length 39;
Best Local Similarity 70.3%; Pred. No. 2.4e+04;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 133 GAGGACCGCGGCTCTGAGATGAGCTGAGGAGGCGGCGG 169
DB 37 GAGGACCGCGGCTCTGAGATGAGCTGAGGAGGCGGCGG 1

RESULT 79

US-08-938-830-30

Sequence 30, Application US/08938830
Patent No. 6040437

GENERAL INFORMATION:
APPLICANT: Laeky, Laurence A.
TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

US-08-938-830-30

Query Match 0.8%; Score 19.4; DB 1; Length 39;
Best Local Similarity 70.3%; Pred. No. 2.4e+04;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 133 GAGGACCGCGGCTCTGAGATGAGCTGAGGAGGCGGCGG 169
DB 37 GAGGACCGCGGCTCTGAGATGAGCTGAGGAGGCGGCGG 1

RESULT 79

US-08-938-830-30

Sequence 30, Application US/08938830
Patent No. 6040437

GENERAL INFORMATION:
APPLICANT: Laeky, Laurence A.
TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

US-08-938-830-30

Query Match 0.8%; Score 19.4; DB 1; Length 39;
Best Local Similarity 70.3%; Pred. No. 2.4e+04;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 133 GAGGACCGCGGCTCTGAGATGAGCTGAGGAGGCGGCGG 169
DB 37 GAGGACCGCGGCTCTGAGATGAGCTGAGGAGGCGGCGG 1

RESULT 79

US-08-938-830-30

Sequence 30, Application US/08938830
Patent No. 6040437

GENERAL INFORMATION:
APPLICANT: Laeky, Laurence A.
TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

US-08-938-830-30

Query Match 0.8%; Score 19.4; DB 1; Length 39;
Best Local Similarity 70.3%; Pred. No. 2.4e+04;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 133 GAGGACCGCGGCTCTGAGATGAGCTGAGGAGGCGGCGG 169
DB 37 GAGGACCGCGGCTCTGAGATGAGCTGAGGAGGCGGCGG 1

RESULT 79

US-08-938-830-30

Sequence 30, Application US/08938830
Patent No. 6040437

GENERAL INFORMATION:
APPLICANT: Laeky, Laurence A.
TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 12-888-98 : polymorphic base G or A
US-09-641-638-1045

Query Match 0.8%; Score 19.4; DB 4; Length 47;
Best Local Similarity 74.2%; Pred. No. 2.6e+04;
Matches 23; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2120 ATAAATATATATTTTCAATAGATTTTGA 2150
DB 1 ATAAATATATTTTGAAGTTTCAATGA 31

RESULT 83
US-08-983-607-5/c
Sequence 5, Application US/08983607
Patent No. 6140470
GENERAL INFORMATION:
APPLICANT: Alan Garen
APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Department of Molecular Biophysics
ADDRESSEE: and Biochemistry, Yale University
STREET: 266 Whitney Avenue
CITY: New Haven
STATE: Connecticut
COUNTRY: United States of America
ZIP: 06520-8114
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,607
FILING DATE: April 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mary M. Krinsky
REGISTRATION/DOCKET NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-679
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544
TELEFAX: 203-773-1183
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 residues
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
DESCRIPTION: primer used in constructs
US-08-983-607-5

Query Match 0.8%; Score 19.4; DB 3; Length 50;
Best Local Similarity 60.5%; Pred. No. 2.7e+04;
Matches 26; Conservative 3; Mismatches 14; Indels 0; Gaps 0;
QY 1501 GCATCGGACCACTTCCATATGACAGCCGAACCTCTGGGCGCAT 1543
DB 43 SCWSCAGCTGACCTGGGCGCACGTCGGCCGGAACCTGAGCGCAT 1

RESULT 84
US-08-983-607-42/c
Sequence 42, Application US/08983607
Patent No. 6140470
GENERAL INFORMATION:
APPLICANT: Alan Garen
APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Department of Molecular Biophysics
ADDRESSEE: and Biochemistry, Yale University
STREET: 266 Whitney Avenue
CITY: New Haven
STATE: Connecticut
COUNTRY: United States of America
ZIP: 06520-8114
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,607
FILING DATE: April 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mary M. Krinsky
REGISTRATION/DOCKET NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-679
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544
TELEFAX: 203-773-1183
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 residues
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
DESCRIPTION: primer used in constructs
US-08-983-607-42

Query Match 0.8%; Score 19.4; DB 3; Length 50;
Best Local Similarity 60.5%; Pred. No. 2.7e+04;
Matches 26; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

QY 1501 GCATCGGACCACTTCCATATGACAGCCGAACCTCTGGGCGCAT 1543
DB 43 SCWSCAGCTGACCTGGGCGCACGTCGGCCGGAACCTGAGCGCAT 1

RESULT 85
US-09-264-737-4
Sequence 4, Application US/09264737A
Patent No. 6107549
GENERAL INFORMATION:
APPLICANT: Feng, Paul C.C.
APPLICANT: Ruff, Thomas G.
TITLE OF INVENTION: Engineering Plant Resistance to Pyridines via
TITLE OF INVENTION: Expression of Esterase Enzymes
FILE REFERENCE: 38-21(10551) RLE3 Pyridine Tolerance
CURRENT APPLICATION NUMBER: US/09/264,737A
FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: 60/077,377
EARLIER FILING DATE: 1998-03-10

NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 55
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: amino terminal degenerate synthetic amplification
OTHER INFORMATION: primer based on published amino acid sequence of
OTHER INFORMATION: rabbit liver esterase isozyme 1 (RLE1 (Ozols, 1987));
US-09-264-737-4

Query Match 0.8%; Score 19.4; DB 3; Length 55;
Best Local Similarity 65.7%; Pred. No. 2.8e+04;
Matches 23; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1270 GCTCCATCTGACTTGAAAGTGGAAGAAAGTT 1304
DB 21 GCACCACCTGTGTGACACTGTNAARGNARGT 55

RESULT 86
US-08-592-406-9/c
Sequence 9, Application US/08592406
Patent No. 5821059
GENERAL INFORMATION:
APPLICANT: MINION, F. Chris
APPLICANT: KNUDSON, Kevin L.
TITLE OF INVENTION: MYOPLASMA EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,406
FILING DATE: 06-FEB-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US93/07407
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 76645/132
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-592-406-9

Query Match 0.8%; Score 19.4; DB 1; Length 60;
Best Local Similarity 60.4%; Pred. No. 3e+04;
Matches 33; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1799 AATGATATGCTGAAGCTTATGACATCAATTAATGATCTCCGACATC 1851
DB 59 ATTGTATCTCAACACTTCGGATATATATATCATCATGATGAATACATC 7

RESULT 87
US-08-741-881-44
Sequence 44, Application US/08741881
Patent No. 5789245
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/741,881
FILING DATE: 30-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McMaisters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049, 42306 / 1146, 007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-741-881-44

Query Match 0.8%; Score 19.2; DB 1; Length 34;
Best Local Similarity 75.0%; Pred. No. 2.5e+04;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2121 TAAATATATATTTTCAATAGATTTTGATT 2152
DB 1 TATATATAGATCTTGACATGATTAATGACT 32

RESULT 88
US-08-739-158-44
Sequence 44, Application US/08739158
Patent No. 581482
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US

ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/739,158
FILING DATE: 30-OCT-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: McMaister, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-739-158-44

Query Match 0.8%; Score 19.2; DB 1; Length 34;
Best Local Similarity 75.0%; Pred. No. 2.5e+04;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2121 TAAATATATATTTTCAATGATTTTGATT 2152
DB 1 TATATATGATCTTGACATGATTATTTGACT 32

RESULT 89
US-08-739-167-44
Sequence 44, Application US/08739167
Patent No. 5843723
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/739,167
FILING DATE: 30-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McMaister, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:

LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-739-167-44

Query Match 0.8%; Score 19.2; DB 2; Length 34;
Best Local Similarity 75.0%; Pred. No. 2.5e+04;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2121 TAAATATATATTTTCAATGATTTTGATT 2152
DB 1 TATATATGATCTTGACATGATTATTTGACT 32

RESULT 90
US-08-404-796-44
Sequence 44, Application US/08404796
Patent No. 6015686
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,796
FILING DATE: 15-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McMaister, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-404-796-44

Query Match 0.8%; Score 19.2; DB 3; Length 34;
Best Local Similarity 75.0%; Pred. No. 2.5e+04;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2121 TAAATATATATTTTCAATGATTTTGATT 2152
DB 1 TATATATGATCTTGACATGATTATTTGACT 32

RESULT 91
US-08-931-869-44
Sequence 44, Application US/08931869
Patent No. 6015694

GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
City: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,869
FILING DATE: 16-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/404,796
FILING DATE: 15-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-931-869-44

Query Match 0.8%; Score 19.2; DB 3; Length 34;
Best Local Similarity 75.0%; Pred. No. 2.5e+04;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2121 TAAATATATATTTTCAATAGATTGATT 2152
Db 1 TATATATGATCTTTGACATGATTATTGACT 32

RESULT 92
US-09-350-399-44
Sequence 44, Application US/09350399
Patent No. 6342372
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
City: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/350,399
FILING DATE: 08-Jul-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-350-399-44

Query Match 0.8%; Score 19.2; DB 4; Length 34;
Best Local Similarity 75.0%; Pred. No. 2.5e+04;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2121 TAAATATATATTTTCAATAGATTGATT 2152
Db 1 TATATATGATCTTTGACATGATTATTGACT 32

RESULT 93
US-09-236-140A-44
Sequence 44, Application US/09236140A
Patent No. 6376236
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: OPPENHEIMER WOLFF & DONNELLY
STREET: 840 NEWPORT CENTER DRIVE, SUITE 700
CITY: NEWPORT BEACH
STATE: CALIFORNIA
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,140A
FILING DATE: 22-Jan-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Cullman, Louis C.
REGISTRATION NUMBER: 39,645
REFERENCE/DOCKET NUMBER: 20263.332 / 1146.020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (949) 823.6000
TELEFAX: (949) 823.6100
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-236-140A-44

Query Match 0.8%; Score 19.2; DB 4; Length 34;
Best Local Similarity 75.0%; Pred. No. 2.5e+04;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2121 TAAATATATATTTTCAATAGATTGATT 2152
DB 1 TATATATAGATCTTGACATTGATTGACT 32

RESULT 94
US-09-415-784-41
Sequence 41, Application US/09415784
Patent No. 6391632
GENERAL INFORMATION:
APPLICANT: Dubensky Jr., Thomas W.
Polo, John M.
Bell, Barbara A.
Schlesinger, Sondra
Dryga, Sergey A.
Frolov, Ilya

TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
SYNTHESIS

NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/415,784
FILING DATE: 08-Oct-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: McMaisters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.457D1 /1196.006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-415-784-41
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-09-415-784-41

Query Match 0.8%; Score 19.2; DB 4; Length 34;
Best Local Similarity 75.0%; Pred. No. 2.5e+04;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2121 TAAATATATATTTTCAATAGATTGATT 2152
DB 1 TATATATAGATCTTGACATTGATTGACT 32

RESULT 95
US-09-415-785A-41
Sequence 41, Application US/09415785A

Patent No. 6426196
GENERAL INFORMATION:
APPLICANT: Dubensky Jr., Thomas W.
Polo, John M.
Bell, Barbara A.
Schlesinger, Sondra
Dryga, Sergey A.
Frolov, Ilya

TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
SYNTHESIS

NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/415,785A
FILING DATE: 08-Oct-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: McMaisters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.457D1 /1196.006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-415-785A-41
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-09-415-785A-41

Query Match 0.8%; Score 19.2; DB 4; Length 34;
Best Local Similarity 75.0%; Pred. No. 2.5e+04;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2121 TAAATATATATTTTCAATAGATTGATT 2152
DB 1 TATATATAGATCTTGACATTGATTGACT 32

RESULT 96
US-08-944-465-41
Sequence 41, Application US/08944465
Patent No. 6451592
GENERAL INFORMATION:
APPLICANT: Dubensky Jr., Thomas W.
Polo, John M.
Bell, Barbara A.
Schlesinger, Sondra
Dryga, Sergey A.
Frolov, Ilya

TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
SYNTHESIS

NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington

COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,465
FILING DATE: 06-Oct-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMaisters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.457C4 / 1196.005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-944-465-41

Query Match 0.8%; Score 19.2; DB 4; Length 34;
Best Local Similarity 75.0%; Pred. No. 2.5e+04;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2121 TAAATATATATTTTCAATGATTTTGACT 2152
Db 1 TATATATGATCTTTGACATGATTATTTGACT 32

RESULT 97
US-09-415-868-41
Sequence 41, Application US/09415868
Patent No. 6458560
GENERAL INFORMATION:
APPLICANT: Dubensky Jr., Thomas W.
APPLICANT: Polo, John M.
APPLICANT: Belli, Barbara A.
APPLICANT: Schlesinger, Sondra
APPLICANT: Dryga, Sergey A.
APPLICANT: Frolov, Ilya
TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
TITLE OF INVENTION: WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/415,868
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/944,465
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: McMaisters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.457C4 / 1196.005

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-415-868-41

Query Match 0.8%; Score 19.2; DB 4; Length 34;
Best Local Similarity 75.0%; Pred. No. 2.5e+04;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2121 TAAATATATATTTTCAATGATTTTGACT 2152
Db 1 TATATATGATCTTTGACATGATTATTTGACT 32

RESULT 98
US-09-415-900-41
Sequence 41, Application US/09415900
Patent No. 6465634
GENERAL INFORMATION:
APPLICANT: Dubensky Jr., Thomas W.
APPLICANT: Polo, John M.
APPLICANT: Belli, Barbara A.
APPLICANT: Schlesinger, Sondra
APPLICANT: Dryga, Sergey A.
APPLICANT: Frolov, Ilya
TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
TITLE OF INVENTION: WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/415,900
FILING DATE: 08-Oct-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMaisters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.457D4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-415-900-41

Query Match 0.8%; Score 19.2; DB 4; Length 34;
Best Local Similarity 75.0%; Pred. No. 2.5e+04;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2121 TAAATATATATTTTCAATGATTTTGACT 2152
Db 1 TATATATGATCTTTGACATGATTATTTGACT 32

RESULT 99
US-09-076-193-1
Sequence 1, Application US/09076193
Patent No. 5973231
GENERAL INFORMATION:
APPLICANT: Bradfisch, Gregory A.
APPLICANT: Muller-Cohn, Judy
APPLICANT: Narva, Kenneth E.
APPLICANT: Fu, Jenny M.
APPLICANT: Thompson, Mark
TITLE OF INVENTION: Bacillus thuringiensis Isolates, Toxins, and
NUMBER OF INVENTION: Genes for Controlling Certain Coleopteran Pests
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 NW 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076,193
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-716
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-076-193-1

Query Match 0.8%; Score 19.2; DB 2; Length 40;
Best Local Similarity 60.0%; Pred. No. 2.7e+04;
Matches 24; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 2240 TGGTGAATATTAATAATGCAATGATCATTTGTTAACA 2279
DB 1 TGGATTAATAATCATWACACATGAGATTAATTAATWAGACA 40

RESULT 100
US-09-605-192-4/C
Sequence 4, Application US/09605192
Patent No. 6323009
GENERAL INFORMATION:
APPLICANT: Dean, Frank B.
APPLICANT: Laskin, Roger S.
APPLICANT: Nelson, John
TITLE OF INVENTION: Multiply-primed Amplification of Nucleic Acid Sequences
FILE REFERENCE: 469290-41
CURRENT APPLICATION NUMBER: US/09/605,192
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 40
TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Oligonucleotide
OTHER INFORMATION: primer that anneals to M13 (+)-strand DNA.
US-09-605-192-4

Query Match 0.8%; Score 19.2; DB 4; Length 40;
Best Local Similarity 67.5%; Pred. No. 2.7e+04;
Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2216 CCAGACACTTCTGTTCTTCTCTGTTGTAATATATATA 2255
DB 40 CCGGCTAATCTAATCTCTCTGAGAAAAAAA 1

Search completed: April 19, 2003, 10:07:20
Job time: 102 secs

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ALIGNMENTS

93 18.8 0.8 53 9 US-10-083-168-92 Sequence 92, Appl
94 18.8 0.8 54 7 US-08-781-986A-2724 Sequence 2724, Ap
95 18.8 0.8 56 10 US-09-944-036-30 Sequence 30, Appl
96 18.8 0.8 57 7 US-08-781-986A-1941 Sequence 1941, Ap
97 18.8 0.8 57 9 US-08-981-803-29 Sequence 29, Appl
98 18.8 0.8 58 10 US-09-878-574-9023 Sequence 9023, Ap
99 18.8 0.8 59 9 US-10-007-968-8 Sequence 8, Appl
100 18.8 0.8 59 9 US-10-007-280A-2 Sequence 2, Appl

RESULT 1

US-08-781-986A-1737
Sequence 1737, Application US/08781986A
Publication No. US2003005436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 1737:
SEQUENCE CHARACTERISTICS:
LENGTH: 57 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-781-986A-1737
Query Match 1.0%; Score 24.2; DB 7; Length 57;
Best Local Similarity 71.1%; Pred. No. 7.4e+03;
Matches 32; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 421 AGAAGTCTAAAGATACAGCTCATACAAAGCAGACGGAATTATT 465
Db 1 AAGAAGCTAAAGAAAGTTGATTAACACGCAAAAGTATTATT 45

RESULT 2
US-09-922-261-231
Sequence 231, Application US/09922261
Patent No. US2002011471A1
GENERAL INFORMATION:
APPLICANT: COSENT NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth

APPLICANT: Portbury, Stuart D.
APPLICANT: Putnam, Kasturi
APPLICANT: Katz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/922,261
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US/09/461,697
PRIOR FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 231
LENGTH: 60
TYPE: DNA
ORGANISM: Homo sapiens
US-09-922-261-231
Query Match 1.0%; Score 23.6; DB 10; Length 60;
Best Local Similarity 64.8%; Pred. No. 1.1e+04;
Matches 35; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1635 AAAAAAGTGAAGAGGAGATGTGTGACATCTTGCAAGTGAACAGACTCAA 1688
Db 7 AAGAAGATGAAGGTGAAATGAGAGAAAGAGCTGCAAAAGAGAAAGATTAA 60

RESULT 3

US-09-925-301-758/C
Sequence 758, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 758
LENGTH: 60
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (36)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (38)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (40)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (45)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (46)
OTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-758

Query Match 1.0%; Score 22.8; DB 10; Length 60;
Best Local Similarity 63.8%; Pred. No. 1.8e+04;
Matches 30; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1756 TTTTAAAAATCAATCATGTGTGCAAAAAAACTTAAAGCAAAATTA 1802
Db 56 TTTTAAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 10

RESULT 4
US-10-033-297-162
; Sequence 162, Application US/10033297
; Publication No. US20020187486A1
; GENERAL INFORMATION:
; APPLICANT: Hall, Jeff G.
; Lyamichev, Victor I.
; Maet, Andrea L.
; Brow, Mary Ann D.
; TITLE OF INVENTION: Detection Of Nucleic Acids By Multiple
; Sequential Invasive Cleavages
; NUMBER OF SEQUENCES: 163
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/033, 297
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/350, 597
; FILING DATE: 09-JUL-1999
; APPLICATION NUMBER: US/08/823, 516
; FILING DATE: 24-MAR-1997
; APPLICATION NUMBER: PCT/US97/01072
; FILING DATE: 21-JAN-1997
; APPLICATION NUMBER: US 08/759, 038
; FILING DATE: 02-DEC-1996
; APPLICATION NUMBER: US 08/758, 314
; FILING DATE: 02-DEC-1996
; APPLICATION NUMBER: US 08/756, 386
; FILING DATE: 29-NOV-1996
; APPLICATION NUMBER: US 08/682, 853
; FILING DATE: 12-JUL-1996
; APPLICATION NUMBER: US 08/599, 491
; FILING DATE: 24-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40, 027
; REFERENCE/DOCKET NUMBER: FORS-02736
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 162:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 162:
US-10-033-297-162
Query Match 1.0%; Score 22.6; DB 9; Length 54;
Best Local Similarity 75.7%; Pred. No. 1.9e+04;
Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 128 AGCCAGAGAGCGGGCTCTGAGATGAGCTGAGGA 164
DB 4 AGGAAGAGAGAGGGTCTCAGAGAGAGCGGAGGA 40

RESULT 5
US-09-940-244-162
; Sequence 162, Application US/09940244
; Publication No. US20030044796A1
; GENERAL INFORMATION:
; APPLICANT: Neri, Bruce P.
; APPLICANT: Hall, Jeff G.
; APPLICANT: Lyamichev, Victor
; APPLICANT: Smith, Lloyd M.
; TITLE OF INVENTION: Reactions on Dendrimers
; FILE REFERENCE: FORS-06478
; CURRENT APPLICATION NUMBER: US/09/940, 244
; CURRENT FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 422
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 162
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-940-244-162
Query Match 1.0%; Score 22.6; DB 9; Length 54;
Best Local Similarity 75.7%; Pred. No. 1.9e+04;
Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 128 AGCCAGAGAGCGGGCTCTGAGATGAGCTGAGGA 164
DB 4 AGGAAGAGAGAGGGTCTCAGAGAGAGCGGAGGA 40

RESULT 6
US-09-983-965-2161
; Sequence 2161, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 37-21 (10297)C
; CURRENT APPLICATION NUMBER: US/09/983, 965
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465, 231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113, 678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 2161
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 40-LIB3057-003-Q1-K1-B8
US-09-983-965-2161
Query Match 1.0%; Score 22.4; DB 10; Length 53;
Best Local Similarity 72.5%; Pred. No. 2.1e+04;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1129 CCCTTTAAACCTCTGTGCAATCTGAAGAGATGTAATC 1168
DB 11 CCCTGTACACATCTTTTCAAACTGGAGAGCCTTCAAGTC 50

RESULT 7
US-09-846-430A-5/C
; Sequence 5, Application US/09846430A
; Publication No. US20030049620A1

GENERAL INFORMATION:
APPLICANT: LAI, Jennifer H.
APPLICANT: PHILLIPS, Vincent
APPLICANT: MATSON, Andrew R
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR POLYNUCLEOTIDE ANALYSIS
TITLE OF INVENTION: USING GENERIC CAPTURE SEQUENCES
FILE REFERENCE: 5100-7001 / 0016-US
CURRENT APPLICATION NUMBER: US/09/846,430A
CURRENT FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: 60/200,635
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 39
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Cc1a-B
US-09-846-430A-5

Query Match 0.9%; Score 22; DB 9; Length 39;
Best Local Similarity 73.7%; Pred. No. 2.2e+04;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1763 AATCAATCAATGTCGCAAAAAAACTTAAGCAAAA 1800
Db 39 AATCAATCAATGTCGCAAAAAAACTTAAGCAAAA 2

RESULT 8
US-08-781-986A-1690
Sequence 1690, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 1690:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-781-986A-1690

Query Match 0.9%; Score 21.8; DB 7; Length 55;

Best Local Similarity 70.7%; Pred. No. 3.1e+04;
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Qy 2174 CCAACTTTAAATGCGAAATTAATGTTGTTGTAAGAAA 2214
Db 1 CCAACTTTAAATGCGAAATGTTGTTGTAATTAAGAAAT 41

RESULT 9
US-09-783-590-2406/C
Sequence 2406, Application US/09783590
Patent No. US2002010850A1
GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William A.
APPLICANT: Li, Haodong
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16,2C1
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2406
LENGTH: 58
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (34)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (41)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (47)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (52)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (58)
OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-2406

Query Match 0.9%; Score 21.8; DB 10; Length 58;
Best Local Similarity 64.4%; Pred. No. 3.3e+04;
Matches 29; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 1758 TTAATAATCAATGTCGCAAAAAAACTTAAGCAAAA 1802
Db 54 TTAATAATTTTAAAGGNNAAAAAATTAAGCAAAA 10

RESULT 10
US-09-801-274-808
Sequence 808, Application US/09801274
Patent No. US20020032319A1
GENERAL INFORMATION:
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Lander, Eric S.
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: 2825-2009-001
CURRENT APPLICATION NUMBER: US/09/801,274
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 60/187,510
PRIOR FILING DATE: 2000-03-07

;; PRIOR APPLICATION NUMBER: US 60/206,129
;; PRIOR FILING DATE: 2000-05-22
;; NUMBER OF SEQ ID NOS: 1802
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 808
;; LENGTH: 31
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-801-274-808

Query Match 0.9%; Score 21.4; DB 10; Length 31;
Best Local Similarity 88.0%; Pred. No. 2.7e+04;
Matches 22; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1777 TGCAGAAAAAACTTAAGCAAAAT 1801
Db 6 TCCAAAAAAARACTTACAGCAAAAT 30

RESULT 11
US-09-877-478-4141
;; Sequence 4141, Application US/09877478
;; Publication No. US20030068301A1
;; GENERAL INFORMATION:
;; APPLICANT: Ribozyme Pharmaceuticals, Inc.
;; APPLICANT: Draper, Kenneth
;; APPLICANT: Blatt, Larry
;; APPLICANT: McSwiggen, Jim
;; APPLICANT: Morrissey, Dave
;; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
;; FILE REFERENCE: MBH800-845-H (400/029)
;; CURRENT APPLICATION NUMBER: US/09/877,478
;; CURRENT FILING DATE: 2001-12-31
;; PRIOR APPLICATION NUMBER: US 07/882,712
;; PRIOR FILING DATE: 1992-05-14
;; PRIOR APPLICATION NUMBER: US 09/531,025
;; PRIOR FILING DATE: 2000-03-20
;; PRIOR APPLICATION NUMBER: US 09/636,385
;; PRIOR FILING DATE: 2000-08-09
;; PRIOR APPLICATION NUMBER: US 09/696,347
;; PRIOR FILING DATE: 2000-10-24
;; PRIOR APPLICATION NUMBER: US 08/193,627
;; PRIOR FILING DATE: 1994-02-07
;; PRIOR APPLICATION NUMBER: US 08/433,993
;; PRIOR FILING DATE: 1995-05-04
;; PRIOR APPLICATION NUMBER: US 08/434,504
;; PRIOR FILING DATE: 1995-05-04
;; PRIOR APPLICATION NUMBER: US 09/436,430
;; PRIOR FILING DATE: 1999-11-08
;; NUMBER OF SEQ ID NOS: 6586
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 4141
;; LENGTH: 37
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-877-478-4141

Query Match 0.9%; Score 21.2; DB 9; Length 37;
Best Local Similarity 58.8%; Pred. No. 3.5e+04;
Matches 20; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 175 TTAAATGAAGCATGACCATGGGGGAGTTGGAC 208
Db 4 TUGAAGUAGUGCAUGCAUCUAGCCGAGUAGGAC 37

RESULT 12
US-09-764-860-203
;; Sequence 203, Application US/09764860
;; Patent No. US20020094953A1
;; GENERAL INFORMATION:

;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;; FILE REFERENCE: PC008
;; CURRENT APPLICATION NUMBER: US/09/764,860
;; CURRENT FILING DATE: 2001-01-17
;; Prior application data removed - consult PAM or file wrapper
;; NUMBER OF SEQ ID NOS: 1198
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 203
;; LENGTH: 58
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-764-860-203

Query Match 0.9%; Score 21.2; DB 10; Length 58;
Best Local Similarity 64.0%; Pred. No. 4.7e+04;
Matches 32; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 2089 TACGTGCAACACACTGAACTTTTATATATAATATTTTCA 2138
Db 8 TATTTCAACATAGAGAACTTTTTTTTTTTTTTTTAAATTTA 57

RESULT 13
US-10-013-737-17
;; Sequence 17, Application US/10013737
;; Patent No. US20020115093A1
;; GENERAL INFORMATION:
;; APPLICANT: Reynolds, Mark A.
;; APPLICANT: Ruvolet, Michael
;; APPLICANT: Arnold, Jr., Lyle J.
;; TITLE OF INVENTION: COMBINED POLYNUCLEOTIDE SEQUENCES AS DISCRETE ASSAY
;; TITLE OF INVENTION: ENDPOINTS
;; FILE REFERENCE: IN-0017 US
;; CURRENT APPLICATION NUMBER: US/10/013,737
;; CURRENT FILING DATE: 2001-11-12
;; PRIOR APPLICATION NUMBER: US/09/532,656
;; PRIOR FILING DATE: 2000-03-20
;; NUMBER OF SEQ ID NOS: 16
;; SOFTWARE: PERL Program
;; SEQ ID NO 17
;; LENGTH: 59
;; TYPE: DNA
;; ORGANISM: Candida albicans
;; FEATURE:
;; NAME/KEY: misc.feature
;; OTHER INFORMATION: Incyte ID No. US20020115093A1 F23S805
US-10-013-737-17

Query Match 0.9%; Score 21; DB 12; Length 59;
Best Local Similarity 66.7%; Pred. No. 5.4e+04;
Matches 30; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1078 TTCTTAGACACATTAAGTGAAGAACTTCTGCTGAAAGGTG 1122
Db 5 TTCTTAGACATTAAGAAAGAAAGAACTGTTTGAAGTGTG 49

RESULT 14
US-09-798-675-21
;; Sequence 21, Application US/09798675
;; Patent No. US20020106798A1
;; GENERAL INFORMATION:
;; APPLICANT: Emory University
;; TITLE OF INVENTION: HIV VACCINES
;; FILE REFERENCE: E056 2020
;; CURRENT APPLICATION NUMBER: US/09/798,675
;; CURRENT FILING DATE: 2001-12-11
;; PRIOR APPLICATION NUMBER: US 60/186,364
;; PRIOR FILING DATE: 2000-03-02
;; PRIOR APPLICATION NUMBER: US 60/251,083
;; PRIOR FILING DATE: 2000-12-01
;; NUMBER OF SEQ ID NOS: 24

SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: E4780 RT5 primer
US-09-798-675-21

Query Match 0.9%; Score 20.8; DB 10; Length 40;
Best Local Similarity 70.0%; Pred. No. 4.7e+04;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 967 CCTACTCACAAGAGCCAGATGCTTAAAGC 1006
Db 1 CCTACTCACAAGAGCCAGATGCTTAAAGC 40

RESULT 15
US-09-798-675-22/c
; Sequence 22, Application US/09798675
; Patent No. US20020106798A1
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: HIV VACCINES
; FILE REFERENCE: E056 2020
; CURRENT APPLICATION NUMBER: US/09/798,675
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 60/186,364
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/251,083
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: E4780 RT6 primer
US-09-798-675-22

Query Match 0.9%; Score 20.8; DB 10; Length 40;
Best Local Similarity 70.0%; Pred. No. 4.7e+04;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 967 CCTACTCACAAGAGCCAGATGCTTAAAGC 1006
Db 40 CCTACTCACAAGAGCCAGATGCTTAAAGC 1

RESULT 16
US-09-377-885A-34
; Sequence 34, Application US/09377885A
; Publication No. US20030050258A1
; GENERAL INFORMATION:
; APPLICANT: Calos, Michele P.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR GENOMIC MODIFICATION
; FILE REFERENCE: STAN-301
; CURRENT APPLICATION NUMBER: US/09/377,885A
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/097,166
; PRIOR FILING DATE: 1998-08-19
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Mus sp.
US-09-377-885A-34

Query Match 0.9%; Score 20.6; DB 9; Length 34;
Best Local Similarity 85.2%; Pred. No. 4.7e+04;

Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 2107 ATCTTTTATATAATATATATTT 2133
Db 6 ATATTATATTATATATATATTT 32

RESULT 17
US-09-931-325A-72/c
; Sequence 72, Application US/09931325A
; Publication No. US20030054337A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: MALARIA IMMUNOGEN AND VACCINE
; FILE REFERENCE: 4564/83503 ICC-103.1
; CURRENT APPLICATION NUMBER: US/09/931,325A
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/225,843
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: USN NOT YET ASSIGND
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Plasmodium falciparum
US-09-931-325A-72

Query Match 0.9%; Score 20.6; DB 9; Length 49;
Best Local Similarity 67.4%; Pred. No. 6e+04;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 423 AAATGCTAAGATACAGCTCATCAAGAGCAAGGATATT 465
Db 44 AAATGCCACCTTACGCTATCCAAAGCCAAACCGATGTT 2

RESULT 18
US-09-983-965-452
; Sequence 452, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nenghing C.
; APPLICANT: Byatt, John C.
; APPLICANT: Mathaiagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 452
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 53-BOVMS1-015-Q1-E1-F10
US-09-983-965-452

Query Match 0.9%; Score 20.6; DB 10; Length 54;
Best Local Similarity 67.4%; Pred. No. 6.5e+04;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1760 AAAAAATCATCATGTGCAAAAAAACTTAAGCAATA 1802
Db 1 AAAAAATCATCATGTGCAAAAAAACTTAAGCAATA 43

```
RESULT 19
; US-09-931-325A-63/c
; Sequence 63, Application US/09911325A
; Publication No. US20030054337A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: MALARIA IMMUNOGEN AND VACCINE
; FILE REFERENCE: 4564/83503 ICC-103.1
; CURRENT APPLICATION NUMBER: US/09/931.325A
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/225,843
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US/09/931.325A
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; TYPE: DNA
; ORGANISM: Plasmodium falciparum
; US-09-931-325A-63

Query Match      0.9%; Score 20.6; DB 9; Length 55;
Best Local Similarity 67.4%; Pred. No. 6.5e+04;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 423 AATGCTAAGATACAGCTCATACAAAGCAAGCAATATT 465
DB 44 AATGCCAACCTTACGCTAATCCAAAGCCAAACCCGAATGTT 2

RESULT 20
; US-09-931-325A-75/c
; Sequence 75, Application US/09911325A
; Publication No. US20030054337A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: MALARIA IMMUNOGEN AND VACCINE
; FILE REFERENCE: 4564/83503 ICC-103.1
; CURRENT APPLICATION NUMBER: US/09/931.325A
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/225,843
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US/09/931.325A
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; TYPE: DNA
; ORGANISM: Plasmodium falciparum
; US-09-931-325A-75

Query Match      0.9%; Score 20.6; DB 9; Length 55;
Best Local Similarity 67.4%; Pred. No. 6.5e+04;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 423 AATGCTAAGATACAGCTCATACAAAGCAAGCAATATT 465
DB 50 AATGCCAACCTTACGCTAATCCAAAGCCAAACCCGAATGTT 8

RESULT 21
; US-09-931-325A-71
; Sequence 71, Application US/09911325A
; Publication No. US20030054337A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: MALARIA IMMUNOGEN AND VACCINE
; FILE REFERENCE: 4564/83503 ICC-103.1
; CURRENT APPLICATION NUMBER: US/09/931.325A
; CURRENT FILING DATE: 2002-02-22
```

```
; PRIOR APPLICATION NUMBER: 60/225,843
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: USSN NOT YET ASSIGND
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Plasmodium falciparum
; US-09-931-325A-71

Query Match      0.9%; Score 20.6; DB 9; Length 57;
Best Local Similarity 67.4%; Pred. No. 6.7e+04;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 423 AATGCTAAGATACAGCTCATACAAAGCAAGCAATATT 465
DB 10 AATGCCAACCTTACGCTAATCCAAAGCCAAACCCGAATGTT 52

RESULT 22
; US-08-781-986A-5031
; Sequence 5031, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5031:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-781-986A-5031

Query Match      0.9%; Score 20.2; DB 7; Length 54;
Best Local Similarity 75.8%; Pred. No. 8.3e+04;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2106 AATCTTTTATTAATAATAATAATTTTCAA 2138
DB 11 AATCTATTTTACTTACTTACTTACTTTTCAA 43

RESULT 23
```

```
US-09-853-526-315
; Sequence 315, Application US/09853526
; Patent No. US20020165345A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilya, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: PROSTATE CANCER GENE
; FILE REFERENCE: GENSET.18CPICP
; CURRENT APPLICATION NUMBER: US/09/853,526
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/338,907
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 08/996,306
; PRIOR FILING DATE: 1997-12-22
; PRIOR APPLICATION NUMBER: 60/099,658
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 09/218,207
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 315
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1..47
; OTHER INFORMATION: polymorphic fragment 99-147-181, variant version of SEQ ID238
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: base G ; A in SEQ ID238
; NAME/KEY: primer bind
; LOCATION: 1..23
; OTHER INFORMATION: potential microsequencing oligo 99-147-181.mis1
; NAME/KEY: primer bind
; LOCATION: 25..47
; OTHER INFORMATION: complement potential microsequencing oligo 99-147-181.mis2
US-09-853-526-315

Query Match          0.9%; Score 20; DB 9; Length 47;
Best Local Similarity 72.2%; Pred. No. 8.5e+04;
Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 397 GTGCTTAAAGCAATGATGTAAGAAATGCTAAA 432
Db 3 GTCATGAAAAAGACATGATGTAAGAAAGAAACTTAA 38

RESULT 24
US-09-901-484A-315
; Sequence 315, Application US/09901484A
; Patent No. US20020119460A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Prostate Cancer Gene
; FILE REFERENCE: GEN-T11XC3D2
; CURRENT APPLICATION NUMBER: US/09/901,484A
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 08/996,306
; PRIOR FILING DATE: 1997-12-22
; PRIOR APPLICATION NUMBER: US 60/099,658
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: US 09/218,207
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 09/338,907
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: US 09/853,526
; PRIOR FILING DATE: 2001-05-11
```

```
NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 315
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1)..(47)
; OTHER INFORMATION: polymorphic fragment 99-147-181, variant version of SEQ ID 238
; NAME/KEY: allele
; LOCATION: (24)..(24)
; OTHER INFORMATION: polymorphic base G, A in SEQ ID 238
; NAME/KEY: primer bind
; LOCATION: (1)..(23)
; OTHER INFORMATION: potential microsequencing oligo 99-147-181.mis1
; NAME/KEY: primer bind
; LOCATION: (25)..(47)
; OTHER INFORMATION: complement potential microsequencing oligo 99-147-181.mis2
US-09-901-484A-315

Query Match          0.9%; Score 20; DB 10; Length 47;
Best Local Similarity 72.2%; Pred. No. 8.5e+04;
Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 397 GTGCTTAAAGCAATGATGTAAGAAATGCTAAA 432
Db 3 GTCATGAAAAAGACATGATGTAAGAAAGAAACTTAA 38

RESULT 25
US-10-085-906-261
; Sequence 261, Application US/10085906
; Publication No. US20030054371A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Paul
; APPLICANT: Ying, Vincent
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
; TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
; FILE REFERENCE: GNN-5343CP2
; CURRENT APPLICATION NUMBER: US/10/085,906
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/126,215
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 09/534,061
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: PCT/US00/07938
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 545
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 261
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-906-261

Query Match          0.9%; Score 20; DB 9; Length 49;
Best Local Similarity 65.9%; Pred. No. 8.7e+04;
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 2111 TTTTATTATTAATATATATATTTTCAATAGATTTTGATTCA 2154
Db 3 TTTATTATTATTATTATTATTATTATTATTATTATTATTATTAA 46

RESULT 26
US-08-781-986A-2757/C
; Sequence 2757, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunesh
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
```


Query Match 0.9%; Score 20; DB 10; Length 56;

Best Local Similarity 65.9%; Pred. No.

Best Local Similarity 65.9%; Pred. No.

Best Local Similarity 58.3%; Pred. No. 1e+05; Indels 25; Gaps 0;
Matches 35; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1741 AAAAATAACGTGATTTTAAAAATCATCATGTCGACAAAAAAGCTTAAGCAAAA 1800
Db 1 AA 60

RESULT 34

US-09-922-261-233
; Sequence 233, Application US/09922261
; Patent No. US2002011471A1
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Putnam, Kaestut
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/922,261
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US/09/461,697
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 233
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-261-233

Query Match 0.8%; Score 19.8; DB 10; Length 48;
Best Local Similarity 63.8%; Pred. No. 9.7e+04;
Matches 30; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1642 TGGAGAGGAGATGTGAGCATCTCTGCAAGTGAACAGACTCAA 1688
Db 2 TGAAGGTGAAATGAGAGAAAGCTGAGAAAAGAGAAAGATTAA 48

RESULT 35

US-09-866-925-129/C
; Sequence 129, Application US/09866925
; Publication No. US2003003965A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.
; TITLE OF INVENTION: ALGORITHMIC DETERMINATION OF FLANKING DNA SEQUENCES THAT
; TITLE OF INVENTION: CONTROL THE EXPRESSION OF SETS OF GENES IN PROKARYOTIC,
; FILE REFERENCE: 3124-Z
; CURRENT APPLICATION NUMBER: US/09/866,925
; CURRENT FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 249
; SOFTWARE: Proprietary
; SEQ ID NO 129
; LENGTH: 55
; TYPE: DNA
; ORGANISM: A. Thaliania
; FEATURE:
; LOCATION: (499376)...(499430)
; OTHER INFORMATION: Chromosome = 2 Strand = positive ConnectionObjectNumber = 430
US-09-866-925-129

Query Match 0.8%; Score 19.8; DB 9; Length 55;
Best Local Similarity 63.8%; Pred. No. 1.1e+05;
Matches 30; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 2089 TAGGTGAAACCACTGAATCTTTTATATATATATATATTTT 2135

Db 54 TATGCGAAAAAAGCTTAATTTTATATATATGATGATATTTT 8

RESULT 36

US-10-085-906-282/C
; Sequence 282, Application US/10085906
; Publication No. US20030054371A1
; GENERAL INFORMATION:
; APPLICANT: Ying, Vincent
; APPLICANT: Wu, Paul
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
; TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
; FILE REFERENCE: GNN-5343CP2
; CURRENT APPLICATION NUMBER: US/10/085,906
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/126,215
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 09/534,061
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: PCT/US00/07938
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 545
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 282
; LENGTH: 59
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-906-282

Query Match 0.8%; Score 19.8; DB 9; Length 59;
Best Local Similarity 60.0%; Pred. No. 1.1e+05;
Matches 33; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 420 AAGAAATGCTAAAGATRCAGCTCATACAAAGCAGAACGAAATTTCTGAGAGAA 474
Db 58 AAGAAAAAGAGAGAGACGAGAGAGGAGAAAAGTGAATAAGATGAGAGAA 4

RESULT 37

US-09-232-785-363/C
; Sequence 363, Application US/09232785
; Publication No. US20030049612A1
; GENERAL INFORMATION:
; APPLICANT: International Paper Co.
; APPLICANT: Echt, Craig S.
; APPLICANT: Nelson, C. Dana
; TITLE OF INVENTION: MICROSATELLITE DNA MARKERS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 4481/1818US1
; CURRENT APPLICATION NUMBER: US/09/232,785
; CURRENT FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: 09/232,884
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 397
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 363
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Pinus taeda L.
US-09-232-785-363

Query Match 0.8%; Score 19.6; DB 9; Length 44;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 2111 TTTTATATATATATATATATTTTCAATAGATTTTGATT 2152
Db 43 TTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATT 2

RESULT 38

RESULT 42
 US-09-878-178-2169/c
 Sequence 2169, Application US/09878178
 Patent No. US20020177552A1
GENERAL INFORMATION:
 APPLICANT: Jiang, Yugu
 APPLICANT: Hartscocker, Susan L.
 APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527
CURRENT APPLICATION NUMBER: US/09/878,178
CURRENT FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 2237
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2169
LENGTH: 57
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(57)
OTHER INFORMATION: n = A,T,C or G
US-09-878-178-2169

Query Match 0.8%; Score 19.6; DB 9; Length 57;
Best Local Similarity 65.1%; Pred. No. 1.2e+05;
Matches 28; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1760 AAAAAATCATCATGTCGCAAAAAAACTTAAGCAATA 1802
Db 54 AAAAAAAAAAAAAAAAAAGGAAAAAAAAAAAAAAAAAGNA 12

RESULT 43
US-10-127-427-7/c
Sequence 7, Application US/10127427
Publication No. US20030051275A1
GENERAL INFORMATION:
APPLICANT: Paul CHRISTOU; Eva STROGER; Rainer FISCHER; Carmen MARTIN-VAQUERO;
Stefan SC
TITLE OF INVENTION: METHODS AND MEANS FOR EXPRESSION OF MAMMALIAN
POLYPEPTIDES
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,427
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/333,527
FILING DATE: <Unknown>
APPLICATION NUMBER: 60/089,322
FILING DATE: June 15, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Mary Anne Schofield
REGISTRATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: KL/UGC 202.1 - JEL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 57
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-127-427-7

Query Match 0.8%; Score 19.6; DB 9; Length 57;
Best Local Similarity 66.7%; Pred. No. 1.2e+05;
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 2110 TTTTATATATATATATATTTTCAATAGATTTTGCAT 2151
Db 50 TTTTATATATATATATATCTCTATTAATCTGATTTGTGT 9

RESULT 44
US-10-146-502-2169/c
Sequence 2169, Application US/10146502
Publication No. US20030069180A1
GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
APPLICANT: Wang, Aijun
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527C2
CURRENT APPLICATION NUMBER: US/10/146,502
CURRENT FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2241
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2169
LENGTH: 57
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 13
OTHER INFORMATION: n = A,T,C or G
US-10-146-502-2169.

Query Match 0.8%; Score 19.6; DB 9; Length 57;
Best Local Similarity 65.1%; Pred. No. 1.2e+05;
Matches 28; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1760 AAAAAATCATCATGTCGCAAAAAAACTTAAGCAATA 1802
Db 54 AAAAAAAAAAAAAAAAAAGGAAAAAAAAAAAAAAAAAGNA 12

RESULT 45
US-09-333-527-7/c
Sequence 7, Application US/09333527
Patent No. US20020078472A1
GENERAL INFORMATION:
APPLICANT: Paul CHRISTOU; Eva STROGER; Rainer FISCHER; Carmen MARTIN-VAQUERO; Stefa
TITLE OF INVENTION: METHODS AND MEANS FOR EXPRESSION OF MAMMALIAN POLYPEPTIDES
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,527
FILING DATE: Concurrently Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/089,322
FILING DATE: June 15, 1998
ATTORNEY/AGENT INFORMATION:

NAME: Mary Anne Schofield
REGISTRATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: KL/JIC 202.1 - JEL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5938
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 57
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-333-527-7

Query Match 0.8%; Score 19.6; DB 10; Length 57;
Best Local Similarity 66.7%; Pred. No. 1.2e+05;
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 2110 TTTTATATATAATATATATTTTCAATAGATTTTGAT 2151
DB 50 TTTTATATATAATCTCTATATAATCTGATTTGTGT 9

RESULT 46
US-10-085-906-66
Sequence 66, Application US/10085906
Publication No. US20030054371A1
GENERAL INFORMATION:
APPLICANT: Ying, Vincent
APPLICANT: Wu, Paul
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
FILE REFERENCE: GNN-5343CP2
CURRENT APPLICATION NUMBER: US/10/085,906
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 60/126,215
PRIOR FILING DATE: 1999-03-25
PRIOR APPLICATION NUMBER: US 09/534,061
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: PCT/US00/07938
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 545
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 66
LENGTH: 54
TYPE: DNA
ORGANISM: Homo sapiens
US-10-085-906-66

Query Match 0.8%; Score 19.4; DB 9; Length 54;
Best Local Similarity 64.4%; Pred. No. 1.3e+05;
Matches 29; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 2108 TCTTTTATATATAATATATATTTTCAATAGATTTTGAT 2152
DB 2 TATTTTGTATATATATATATATTTTATTTTATTTATTTAAT 46

RESULT 47
US-09-983-965-452/C
Sequence 452, Application US/09983965
Patent No. US20020137160A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengding
APPLICANT: Byatt, John C.
APPLICANT: Mathalagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 37-21(10297)C
CURRENT APPLICATION NUMBER: US/09/983,965
CURRENT FILING DATE: 2001-10-26

PRIOR APPLICATION NUMBER: US 09/465,231
PRIOR FILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: US 60/113,678
PRIOR FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 5912
SEQ ID NO 452
LENGTH: 54
TYPE: DNA
ORGANISM: Bos taurus
FEATURE:
OTHER INFORMATION: Clone ID: 53-BOWMS1-015-Q1-E1-F10
US-09-983-965-452

Query Match 0.8%; Score 19.4; DB 10; Length 54;
Best Local Similarity 64.4%; Pred. No. 1.3e+05;
Matches 29; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 2108 TCTTTTATATATAATATATATTTTCAATAGATTTTGAT 2152
DB 47 TTTTATATATAATCTCTATATAATCTGATTTGTGT 3

RESULT 48
US-09-263-959-519
Sequence 519, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSER: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMaisters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 519:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-519

Query Match 0.8%; Score 19.4; DB 10; Length 54;
Best Local Similarity 64.4%; Pred. No. 1.3e+05;
Matches 29; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1762 AAAATCAATCATGTCGCAAAAAAATTAAGCAAAATAGTAT 1806
DB 1 AAAATAAACCAAAATAAATAAATAAATAAATAAATAAAT 45

RESULT 49

```
US-10-046-935-335/c
; Sequence 335, Application US/10046935
; Patent No. US20020156011A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugui
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.527C1
; CURRENT APPLICATION NUMBER: US/10/046,935
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 2239
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 335
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 10..13
; OTHER INFORMATION: n = A,T,C or G
US-10-046-935-335.

Query Match          0.8%; Score 19.4; DB 9; Length 60;
Best Local Similarity 58.2%; Pred. No. 1.4e+05;
Matches 32; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 1756 TTTTAAATCAATCATGTGCAAAAAAAGCTTAAGCAAAATGATTTGCT 1810
Db 60 TTTTAAACCAAAAAAATATAAAAAATAAAAAANAAAGCT 6

RESULT 50
US-09-878-178-335/c
; Sequence 335, Application US/09878178
; Patent No. US2002017552A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugui
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.527
; CURRENT APPLICATION NUMBER: US/09/878,178
; CURRENT FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 2237
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 335
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(60)
; OTHER INFORMATION: n = A,T,C or G
US-09-878-178-335.

Query Match          0.8%; Score 19.4; DB 9; Length 60;
Best Local Similarity 58.2%; Pred. No. 1.4e+05;
Matches 32; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 1756 TTTTAAATCAATCATGTGCAAAAAAAGCTTAAGCAAAATGATTTGCT 1810
Db 60 TTTTAAACCAAAAAAATATAAAAAATAAAAAANAAAGCT 6

RESULT 51
US-10-208-155-6
; Sequence 6, Application US/10208155
; Publication No. US20030013171A1
```

```
GENERAL INFORMATION:
; APPLICANT: Yang et al.
; TITLE OF INVENTION: BCL-X[SYMBOL 103 \f "Symbol"], A NOVEL BCL-X
; ISOFORM, AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/208,155
; FILING DATE: 29-Jul-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,367
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-208-155-6

Query Match          0.8%; Score 19.4; DB 9; Length 60;
Best Local Similarity 70.3%; Pred. No. 1.4e+05;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 150 GGATGAGCTGAGAGGGGGCTCACTTAATGAAGC 186
Db 2 GGGTGATGTGAGCTGGGATGTCAGTCACTGAATGC 38

RESULT 52
US-10-146-502-335/c
; Sequence 335, Application US/10146502
; Publication No. US20030069180A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugui
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.527C2
; CURRENT APPLICATION NUMBER: US/10/146,502
; CURRENT FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 335
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 10..13
```

NAME: Williams, Joseph A., Jr.
REGISTRATION NUMBER: 38 659

REFERENCE/DOCKET NUMBER: 33282
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 101:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 43 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US-09-753-436-101

Query Match 0.8%; Score 19.2; DB 10; Length 43;
 Best Local Similarity 67.5%; Pred. No. 1.4e+05;
 Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 189 GGACCATGCGGAGCTGACCATGACCTTGACATGGA 228
 Db 40 GGACCAAGCTGGAGCTGAACGTAAAGTAAGTCAATGCA 1

RESULT 56
 US-09-263-959-148/c
 Sequence 148, Application US/09263959
 Patent No. US20020150891A1
 GENERAL INFORMATION:
 APPLICANT: Hood, Leroy E.
 APPLICANT: Rowen, Lee
 APPLICANT: Koop, Ben F.
 TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
 NUMBER OF SEQUENCES: 1279
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Seed and Berry LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: US
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/263,959
 FILING DATE: 05-MAR-1999
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Mcmasters, David D.
 REGISTRATION NUMBER: 33,963
 REFERENCE/DOCKET NUMBER: 920010.426C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 148:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 46 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-263-959-148

Query Match 0.8%; Score 19.2; DB 10; Length 46;
 Best Local Similarity 87.5%; Pred. No. 1.4e+05;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1911 AGATGTTGCTCTGATCACTGTG 1934
 Db 24 AGATGTTGCTCTGATCACTGTG 1

RESULT 57
 US-09-999-724-14
 Sequence 14, Application US/09999724
 Publication No. US20030022355A1
 GENERAL INFORMATION:
 APPLICANT: WICKHAM, THOMAS J.
 APPLICANT: Kovesdi, Imre
 APPLICANT: BROUGH, DOUGLAS E.
 TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER
 FILE REFERENCE: 212960
 CURRENT APPLICATION NUMBER: US/09/999,724
 CURRENT FILING DATE: 2001-10-24
 PRIOR APPLICATION NUMBER: US 09/101,751
 PRIOR FILING DATE: 1999-01-29
 PRIOR APPLICATION NUMBER: WO 96US19150
 PRIOR FILING DATE: 1996-11-27
 PRIOR APPLICATION NUMBER: US 08/700,846
 PRIOR FILING DATE: 1996-08-21
 PRIOR APPLICATION NUMBER: US 08/701,124
 PRIOR FILING DATE: 1996-08-21
 PRIOR APPLICATION NUMBER: US 08/563,368
 PRIOR FILING DATE: 1995-11-28
 NUMBER OF SEQ ID NOS: 94
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 14
 LENGTH: 48
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic
 US-09-999-724-14

Query Match 0.8%; Score 19.2; DB 9; Length 48;
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;
 Matches 24; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

Qy 1761 AAAATCATCAATGCTGCAAAAAAACTTAAGCAAAA 1800
 Db 8 AAAAAAGAACGUGUGUAAAAAAGAAAAA 47

RESULT 58
 US-09-796-679-18/c
 Sequence 18, Application US/09796679
 Publication No. US2003003076A1
 GENERAL INFORMATION:
 APPLICANT: Robinson, Anthony J
 APPLICANT: Lytle, David J
 APPLICANT: University of Otago
 TITLE OF INVENTION: Parapoxvirus vectors
 FILE REFERENCE: 23607 MRB
 CURRENT APPLICATION NUMBER: US/09/796,679
 CURRENT FILING DATE: 2001-03-30
 PRIOR APPLICATION NUMBER: 09/155,421
 PRIOR FILING DATE: 1998-09-29
 PRIOR APPLICATION NUMBER: PCT/NZ97/00040
 PRIOR FILING DATE: 1997-03-27
 PRIOR APPLICATION NUMBER: NZ 286284
 PRIOR FILING DATE: 1996-03-29
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 18
 LENGTH: 49
 TYPE: DNA
 ORGANISM: Oxf virus strain NZ-2
 US-09-796-679-18

Query Match 0.8%; Score 19.2; DB 9; Length 49;
 Best Local Similarity 67.5%; Pred. No. 1.4e+05;
 Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 Qy 2177 AACTTAAATGCAATTAATGTTGTTGTTGAAGAAAGC 2216
 Db 2177 AACTTAAATGCAATTAATGTTGTTGTTGAAGAAAGC 2216

DB 48 ATCTTTATGTCAGAAATTATTCGTGGCGGAGCTGCG 9

RESULT 59

US-10-085-906-204/c
Sequence 204, Application US/10085906
Publication No. US20030054371A1
GENERAL INFORMATION:
APPLICANT: Ying, Vincent
APPLICANT: Wu, Paul
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
FILE REFERENCE: GNN-5343CP2
CURRENT APPLICATION NUMBER: US/10/085,906
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 60/126,215
PRIOR FILING DATE: 1999-03-25
PRIOR APPLICATION NUMBER: US 09/534,061
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: PCT/US00/07938
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 545
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 204
LENGTH: 49
TYPE: DNA
ORGANISM: Homo sapiens
US-10-085-906-204

Query Match 0.8%; Score 19.2; DB 9; Length 49;
Best Local Similarity 67.8%; Pred. No. 1.4e+05;
Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 911 GCGGATAGAGAAACAATGACAAATCCTCAATG 950

DB 41 GAGGAGAAAGAGAGAAAAAGATGAAAAACATPAAAAAG 2

RESULT 60

US-09-907-900-52/c
Sequence 52, Application US/09907900
Patent No. US2002017297A1
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850004
CURRENT APPLICATION NUMBER: US/09/907,900
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 09/177,387
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 52
LENGTH: 53
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: oligonucleotide
US-09-907-900-52

Query Match 0.8%; Score 19.2; DB 9; Length 53;
Best Local Similarity 75.0%; Pred. No. 1.5e+05;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2009 AATTAGCATGACAGCTTGTCACAACTTTGCC 2040

DB 33 AATTAGCTGCTTTTGTGTACAACTTGTCGCC 2

RESULT 61

US-09-907-719-52/c
Sequence 52, Application US/09907719
Publication No. US20020192819A1
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Rex, Donna K.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850004
CURRENT APPLICATION NUMBER: US/09/907,719
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US/09/177,387
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 52
LENGTH: 53
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: oligonucleotide
US-09-907-719-52

Query Match 0.8%; Score 19.2; DB 9; Length 53;
Best Local Similarity 75.0%; Pred. No. 1.5e+05;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2009 AATTAGCATGACAGCTTGTCACAACTTTGCC 2040

DB 33 AATTAGCTGCTTTTGTGTACAACTTGTCGCC 2

RESULT 62

US-09-855-797A-52/c
Sequence 52, Application US/09855797A
Patent No. US20020094574A1
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850008
CURRENT APPLICATION NUMBER: US/09/855,797A
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/296,281
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: US 60/065,930
PRIOR FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 52
LENGTH: 53
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: oligonucleotide
US-09-855-797A-52

Query Match 0.8%; Score 19.2; DB 10; Length 53;
Best Local Similarity 75.0%; Pred. No. 1.5e+05;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2009 AATTAGCATGACAGCTTGTCACAACTTTGCC 2040

DB 33 AATTAGCTGCTTTTGTGTACAACTTGTCGCC 2

Db 33 AATTAGCCTGCTTTTGTACAACTGTCC 2

RESULT 63

US-09-970-308-8
; Sequence 8, Application US/09970308
; Patent No. US20020045193A1
; GENERAL INFORMATION:
; APPLICANT: BRIZZARD, BILLY L.
; APPLICANT: HERNAN, RON
; TITLE OF INVENTION: PURIFICATION OF RECOMBINANT PROTEINS FUSED TO MULTIPLE
; FILE REFERENCE: SGM 6933.2
; CURRENT APPLICATION NUMBER: US/09/970,308
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 09/415,000
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-970-308-8

Query Match 0.8%; Score 19.2; DB 10; Length 54;

Best Local Similarity 67.5%; Pred. No. 1.5e+05;
Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 377 GGAATATTTGCGATGAGTGTCTTAAAAAGCATGAT 416

Db 15 GGACTACAAAGACCATGCGGTGATTATAAAGATCATGAT 54

RESULT 64

US-09-970-308-9/c
; Sequence 9, Application US/09970308
; Patent No. US20020045193A1
; GENERAL INFORMATION:
; APPLICANT: BRIZZARD, BILLY L.
; APPLICANT: HERNAN, RON
; TITLE OF INVENTION: PURIFICATION OF RECOMBINANT PROTEINS FUSED TO MULTIPLE
; FILE REFERENCE: SGM 6933.2
; CURRENT APPLICATION NUMBER: US/09/970,308
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 09/415,000
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-970-308-9

Query Match 0.8%; Score 19.2; DB 10; Length 54;

Best Local Similarity 67.5%; Pred. No. 1.5e+05;
Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 377 GGAATATTTGCGATGAGTGTCTTAAAAAGCATGAT 416

Db 40 GGACTACAAAGACCATGCGGTGATTATAAAGATCATGAT 1

RESULT 65

US-09-426-548-41
; Sequence 41, Application US/09426548
; Patent No. US20010044936A1

; GENERAL INFORMATION:

; APPLICANT: Robbins, David
; APPLICANT: Lin-Goerke, Julie L.
; APPLICANT: Ling, Jessica
; TITLE OF INVENTION: No. US20010044936A1el Mutations in Human MLH1 and MSH2 Genes Usefi
; FILE REFERENCE: DEX-0054
; CURRENT APPLICATION NUMBER: US/09/426,548
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-426-548-41

Query Match 0.8%; Score 19.2; DB 10; Length 57;

Best Local Similarity 67.5%; Pred. No. 1.6e+05;
Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2117 TATTAATATATATTTTCAATAGATTGATTCAGC 2156

Db 15 TATTAATATATATTTTCAATAGATTGATTCAGTTCATC 54

RESULT 66

US-09-902-941-2002
; Sequence 2002, Application US/09902941
; Patent No. US20020172952A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tonglong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Panger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C17
; CURRENT APPLICATION NUMBER: US/09/902,941
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 2002
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2002
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-902-941-2002

Query Match 0.8%; Score 19.2; DB 9; Length 60;

Best Local Similarity 58.9%; Pred. No. 1.6e+05;
Matches 33; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 652 TTACATCAAAAGGATCATCTACAGAGACCTGAACCCGAGATATCATGCTTAA 707

Db 2 TAATACCTAAGAGAACTGTAATATGCAAGAGAGTGAAGACCAACCA 57

RESULT 67

US-10-017-754-2002
; Sequence 2002, Application US/10017754
; Publication No. US20030054363A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tonglong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.

APPLICANT: Retter, Marc W.
APPLICANT: Marnierakis, Margarita
APPLICANT: Carter, Derrick
APPLICANT: Fanger, Gary R.
APPLICANT: Vedavick, Thomas S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: McNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C18
CURRENT APPLICATION NUMBER: US/10/017,754
CURRENT FILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 2004
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2002
LENGTH: 60
TYPE: DNA
ORGANISM: Homo sapiens
US-10-017-754-2002

Query Match 0.8%; Score 19.2; DB 9; Length 60;
Best Local Similarity 58.9%; Pred. No. 1.6e+05;
Matches 33; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 652 TTACATCAAAAGGGGATCATCTACAGAGACCTGAAGCCGAGAAATATCATGCTTAA 707
Db 2 TAAATACCTAAAGAGAACACTGTAAATGCGAGAGAGGTGAAGACACACACA 57

RESULT 68
US-10-085-906-255/c
Sequence 255, Application US/10085906
Publication No. US2003005437A1
GENERAL INFORMATION:
APPLICANT: Ying, Vincent
APPLICANT: Wu, Paul
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
FILE REFERENCE: GNN-5343CP2
CURRENT APPLICATION NUMBER: US/10/085,906
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 60/126,215
PRIOR FILING DATE: 1999-03-25
PRIOR APPLICATION NUMBER: US 09/534,061
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: PCT/US00/07938
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 545
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 255
LENGTH: 46
TYPE: DNA
ORGANISM: Homo sapiens
US-10-085-906-255

Query Match 0.8%; Score 19; DB 9; Length 46;
Best Local Similarity 65.1%; Pred. No. 1.5e+05;
Matches 28; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 2110 TTTTATATATAATATATATTTTCAATAGATTTTGATT 2152
Db 43 TTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1

RESULT 69
US-09-827-289-20
Sequence 20, Application US/09827289
Patent No. US20020009716A1
GENERAL INFORMATION:
APPLICANT: Abartzua, Patricia
TITLE OF INVENTION: Process for Allele Discrimination Using Primer
TITLE OF INVENTION: Extension

FILE REFERENCE: 469290-55
CURRENT APPLICATION NUMBER: US/09/827,289
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: U.S. 60/194843
PRIOR FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 46
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: P1 primer for
OTHER INFORMATION: use in allele discrimination
US-09-827-289-20

Query Match 0.8%; Score 19; DB 10; Length 46;
Best Local Similarity 65.1%; Pred. No. 1.5e+05;
Matches 28; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 2111 TTTTATATATAATATATATTTTCAATAGATTTTGATT 2153
Db 1 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 43

RESULT 70
US-09-827-289-24
Sequence 24, Application US/09827289
Patent No. US20020009716A1
GENERAL INFORMATION:
APPLICANT: Abartzua, Patricia
TITLE OF INVENTION: Process for Allele Discrimination Using Primer
TITLE OF INVENTION: Extension
FILE REFERENCE: 469290-55
CURRENT APPLICATION NUMBER: US/09/827,289
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: U.S. 60/194843
PRIOR FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 24
LENGTH: 46
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: P1 primer for
OTHER INFORMATION: use in allele discrimination
US-09-827-289-24

Query Match 0.8%; Score 19; DB 10; Length 46;
Best Local Similarity 65.1%; Pred. No. 1.5e+05;
Matches 28; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 2111 TTTTATATATAATATATATTTTCAATAGATTTTGATT 2153
Db 1 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 43

RESULT 71
US-09-938-842A-3904
Sequence 3904, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCDP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 3904
LENGTH: 53
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842a-3904

Query Match 0.8%; Score 19; DB 9; Length 53;
Best Local Similarity 71.4%; Pred. No. 1.7e+05;
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 2085 GTTTACGTGCAACACCTGATCTTTTAT 2119
Db 1 GTATTCTAAAGAAAGAACTGAAATGTTTTTTT 35

RESULT 72
US-09-263-959-519/c
Sequence 519, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMaster, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 519:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-519

Query Match 0.8%; Score 19; DB 10; Length 54;
Best Local Similarity 65.1%; Pred. No. 1.7e+05;
Matches 28; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 2110 TTTTATATATATATATATTTTCAATAGATTTTGAT 2152
Db 53 TTTATTTATTTATTTATTTATTTATTTATTTATTT 11

RESULT 73
US-10-085-906-18/c

Sequence 18, Application US/10085906
Publication No. US20030054371A1
GENERAL INFORMATION:
APPLICANT: Ying, Vincent
APPLICANT: Wu, Paul
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
FILE REFERENCE: GNN-5343CP2
CURRENT APPLICATION NUMBER: US/10/085,906
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 60/126,215
PRIOR FILING DATE: 1999-03-25
PRIOR APPLICATION NUMBER: US 09/534,061
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: PCT/US00/07938
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 545
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18
LENGTH: 55
TYPE: DNA
ORGANISM: Homo sapiens
US-10-085-906-18

Query Match 0.8%; Score 19; DB 9; Length 55;
Best Local Similarity 81.5%; Pred. No. 1.7e+05;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2045 AAAATGGAGCAACACCAAGAAA 2071
Db 38 AAAAAGAAAGAAAGAAAGAAA 12

RESULT 74
US-10-007-132-59/c
Sequence 59, Application US/10007132
Publication No. US20030027254A1
GENERAL INFORMATION:
APPLICANT: Bard, Jonathan A
APPLICANT: Borowsky, Beth
APPLICANT: Smith, Kelli E
TITLE OF INVENTION: DNA ENCODING GALANIN GALR3 RECEPTORS
AND USES THEREOF
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/007,132
FILING DATE: 03-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/058,333
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52241-E/JPW/XDB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 278 0400
TELEFAX: 212 391 0525
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:

LENGTH: 57 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-10-007-132-59

Query Match 0.8%; Score 19; DB 9; Length 57;
Best Local Similarity 71.4%; Pred. No. 1.8e+05;
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1768 AATCAATGTCGCAAAAAAATTAAAGCAAAATA 1802
Db 47 AATAAACCCCTCCAAAAAATAAAAAAAAAAAAAA 13

RESULT 75
US-09-944-036-31/c
Sequence 31, Application US/09944036
Patent No. US20020055095A1
GENERAL INFORMATION:
APPLICANT: YANG, Yeasing Y.
APPLICANT: BRENTANO, Steven T.
APPLICANT: BABOLA, Odile
APPLICANT: TRAN, Nathalie
APPLICANT: VERNET, Guy
TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
FILE REFERENCE: GP14-02.UT
CURRENT APPLICATION NUMBER: US/09/944,036
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,790
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
LENGTH: 57
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Capture
OTHER INFORMATION: Oligonucleotide
US-09-944-036-31

Query Match 0.8%; Score 19; DB 10; Length 57;
Best Local Similarity 65.1%; Pred. No. 1.8e+05;
Matches 28; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 2108 TCTTTTATATATATATATATTTTCAATGATTTTGA 2150
Db 56 TTTTATTTTTTTTTTTTTTTTTTTTAAACGGTTATTA 14

RESULT 76
US-09-943-286-7/c
Sequence 7, Application US/09943286
Patent No. US2002010668A1
GENERAL INFORMATION:
APPLICANT: Nunomura, Kiyotada
TITLE OF INVENTION: POLYNUCLEOTIDE AMPLIFICATION METHOD
FILE REFERENCE: GP104-02.UT
CURRENT APPLICATION NUMBER: US/09/943,286
CURRENT FILING DATE: 2001-08-30
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 57
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Sequence of the (-)-4258 A30 capture probe.

US-09-943-286-7
Query Match 0.8%; Score 19; DB 10; Length 57;
Best Local Similarity 65.1%; Pred. No. 1.8e+05;
Matches 28; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 2108 TCTTTTATATATATATATATTTTCAATGATTTTGA 2150
Db 56 TTTTATTTTTTTTTTTTTTTTTTTTAAACGGTTATTA 14

RESULT 77
US-09-954-692-17
Sequence 17, Application US/09954692
Publication No. US20030027156A1
GENERAL INFORMATION:
APPLICANT: Patten, Phillip
APPLICANT: Stemmer, William P.C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR POLYPEPTIDE ENGINEERING
FILE REFERENCE: 02-020500US
CURRENT APPLICATION NUMBER: US/09/954,692
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US/08/769,062
PRIOR FILING DATE: 1996-12-18
PRIOR APPLICATION NUMBER: 08/425,684
PRIOR FILING DATE: 1995-04-18
PRIOR APPLICATION NUMBER: 08/537,874
PRIOR FILING DATE: 1995-10-30
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 60
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: degenerate
OTHER INFORMATION: Oligonucleotide used for codon usage library
US-09-954-692-17

Query Match 0.8%; Score 19; DB 9; Length 60;
Best Local Similarity 57.1%; Pred. No. 1.8e+05;
Matches 28; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 144 CTCTGAGATGACCTGAGAGGCGGTCAGTTAAATGAAGCATGGAC 192
Db 4 CTCTGAGCTGACCTGCGCSCDCAATGACGTTGCACAGAC 52

RESULT 78
US-09-559-671A-17
Sequence 17, Application US/09559671A
Patent No. US20020051976A1
GENERAL INFORMATION:
APPLICANT: Patten, Phillip
APPLICANT: Stemmer, William P.C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR POLYPEPTIDE ENGINEERING
FILE REFERENCE: 02-020503US
CURRENT APPLICATION NUMBER: US/09/559,671A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 08/769,062
PRIOR FILING DATE: 1996-12-18
PRIOR APPLICATION NUMBER: 08/198,431
PRIOR FILING DATE: 1994-02-17
PRIOR APPLICATION NUMBER: 08/425,684
PRIOR FILING DATE: 1995-04-18
PRIOR APPLICATION NUMBER: 08/537,874
PRIOR FILING DATE: 1995-10-30
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 60
TYPE: DNA
ORGANISM: Artificial Sequence

```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: degenerate
; OTHER INFORMATION: oligonucleotide used for codon usage library
US-09-559-671A-17

```

Query Match Similarity 0.8%; Score 19; DB 10; Length 60;
 Best Local Similarity 57.1%; Pred. No. 1.8e+05;
 Matches 28; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

RESULT 79
 US-09-877-478-4121
 : Sequence 4121, Application US/09877478
 : Publication No. US20030068301A1
 : GENERAL INFORMATION:
 : APPLICANT: Ribozyme Pharmaceuticals, Inc.
 : APPLICANT: Draper, Kenneth
 : APPLICANT: Blatt, Larry
 : APPLICANT: McSwiggen, Jim
 : APPLICANT: Morrissey, Dave
 : TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
 : FILE REFERENCE: MBH00-845-H (400/029)
 : CURRENT APPLICATION NUMBER: US/09/877,478
 : CURRENT FILING DATE: 2001-12-31
 : PRIOR APPLICATION NUMBER: US 07/882,712

OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

RESULT 80
US-09-877-478-3202
; Sequence 3202, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Rhozyme Pharmaceuticals, Inc
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McGswigen, Jim
; APPLICANT: Morrissey, Dave

```

1  TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
2  FILE REFERENCE: MBH00-845-H (400/029)
3  CURRENT APPLICATION NUMBER: US/09/877,478
4  CURRENT FILING DATE: 2001-12-31
5  PRIOR APPLICATION NUMBER: US 07/882,712
6  PRIOR FILING DATE: 1992-05-14
7  PRIOR APPLICATION NUMBER: US 09/531,025
8  PRIOR FILING DATE: 2000-03-20
9  PRIOR APPLICATION NUMBER: US 09/636,385
10 PRIOR FILING DATE: 2000-08-09
11 PRIOR APPLICATION NUMBER: US 09/696,347
12 PRIOR FILING DATE: 2000-10-24
13 PRIOR APPLICATION NUMBER: US 08/193,627
14 PRIOR FILING DATE: 1994-02-07
15 PRIOR APPLICATION NUMBER: US 08/433,993
16 PRIOR FILING DATE: 1995-05-04
17 PRIOR APPLICATION NUMBER: US 08/434,504
18 PRIOR FILING DATE: 1995-05-04
19 PRIOR APPLICATION NUMBER: US 09/436,430
20 PRIOR FILING DATE: 1999-11-08
21 NUMBER OF SEQ ID NOS: 6586
22 SOFTWARE: PatentIn version 3.0
23 SEQ ID NO 3202
24 LENGTH: 38
25 TYPE: RNA
26 ORGANISM: Artificial Sequence
27 FEATURE:
28 OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
29 US-09-877-478-3202
30
31 Query Match 0.8%; Score 18.8; DB 9; Length 38;
32 Best Local Similarity 55.3%; Pred. No. 1.5e+05;
33 Matches 21; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

```

	Query Match	Score	DB %	Length
Best Local Similarity	50.8%	18.9	5.3%	38
Matches	21	Conservative	5	Mismatches 12; Indels 0; Gaps 0
Oy	557	GAGCAGACCTATTATGCAATTGAAAGAGAGGGGATA	594	
Db	1	GUGGAGAUCTUAGAGCCGUTUAGGCCCAAGAGGGAGUA	38	

```

RESULT 81
US-09-247--890-14
Sequence 14, Application US/09247890
Publication No. US20020198162A1
GENERAL INFORMATION:
APPLICANT: Punnonen, Juha
APPLICANT: Bass, Steven H.
APPLICANT: Whalen, Robert Gerald
APPLICANT: Howard, Russell
APPLICANT: Stemmer, Willem P.C.
APPLICANT: Maxygen, Inc.
TITLE OF INVENTION: Antigen Library Immunization
FILE REFERENCE: 018097-028710US
CURRENT APPLICATION NUMBER: US/09/247,890
CURRENT FILING DATE: 1999-02-10
EARLIER APPLICATION NUMBER: US 60/074,294
EARLIER FILING DATE: 1998-02-11
EARLIER APPLICATION NUMBER: US 60/105,509
EARLIER FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 39
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:reverse HBV ayyw
US-09-247--890-14

```

Query Match	0.8%	Score 18.8	DB 9	Length 39
Best Local Similarity	76.7%	Pred. No. 1.6e+05		
Matches 23	Conservative	0	Mismatches 7	Indels 0
				Gaps 0

QY 2050 GGGAAGGCAAGACAAAGAACTTACCAG 2079
Db 4 GGATACCAAGACAAAGAAATGTTAA 33

RESULT 82

US-10-043-573-131/c
; Sequence 131, Application US/10043573
; Publication No. US20030032025A1
; GENERAL INFORMATION:

APPLICANT: Lemieux, Bertrand

Landry, Benoit S.

Sapolsky, Ronald J.

TITLE OF INVENTION: Brassica Polymorphisms

NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/043,573

FILING DATE: 09-Jan-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/813,507

FILING DATE: 07-MAR-1997

APPLICATION NUMBER: US 60/032,069

FILING DATE: 02-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Liebeschuetz, Joe

REGISTRATION NUMBER: 37,505

REFERENCE/DOCKET NUMBER: 018547-031000US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415 576-0200

TELEFAX: 415 576-0200

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 131:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 131:

US-10-043-573-131

Query Match

Best local Similarity 0.8%; Score 18.8; DB 9; Length 42;

Matches 26; Conservative 2; Mismatches 14; Indels 0; Gaps 0;

QY 757 ATTGATGATGACACGACACACATTTTGTGGAACAAAT 798

Db 42 ATGATGCAACACACAGTCACMACACATGTCGTATACATA 1

RESULT 83

US-10-046-935-34/c

; Sequence 34, Application US/10046935

; Patent No. US20020156011A1

; GENERAL INFORMATION:

APPLICANT: Jiang, Yugu

APPLICANT: Harlocker, Susan L.

APPLICANT: Wang, Aijun

APPLICANT: Secretist, Heather

APPLICANT: Stolk, John A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER

; FILE REFERENCE: 210121.527C1

; CURRENT APPLICATION NUMBER: US/10/046,935

; CURRENT FILING DATE: 2002-01-15

; NUMBER OF SEQ ID NOS: 2239

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 34

; LENGTH: 51

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-046-935-34

Query Match

Best local Similarity 0.8%; Score 18.8; DB 9; Length 51;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 430 AAAGTACAGCTCATCAAG 451

Db 22 AAAGCCACAGCTCATCAAG 1

RESULT 84

US-09-878-178-34/c

; Sequence 34, Application US/09878178

; Patent No. US20020177552A1

; GENERAL INFORMATION:

APPLICANT: Jiang, Yugu

APPLICANT: Harlocker, Susan L.

APPLICANT: Secretist, Heather

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.527

; CURRENT APPLICATION NUMBER: US/09/878,178

; CURRENT FILING DATE: 2001-06-08

; NUMBER OF SEQ ID NOS: 2237

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 34

; LENGTH: 51

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-878-178-34

Query Match

Best local Similarity 0.8%; Score 18.8; DB 9; Length 51;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 430 AAAGTACAGCTCATCAAG 451

Db 22 AAAGCCACAGCTCATCAAG 1

RESULT 85

US-10-146-502-34/c

; Sequence 34, Application US/10146502

; Publication No. US20030069180A1

; GENERAL INFORMATION:

APPLICANT: Jiang, Yugu

APPLICANT: Harlocker, Susan L.

APPLICANT: Secretist, Heather

APPLICANT: Wang, Aijun

APPLICANT: Stolk, John A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.527C2

; CURRENT APPLICATION NUMBER: US/10/146,502

; CURRENT FILING DATE: 2002-05-14

; NUMBER OF SEQ ID NOS: 2241

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 34

; LENGTH: 51

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-146-502-34

Query Match

Best local Similarity 0.8%; Score 18.8; DB 9; Length 51;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 430 AAAGTACAGCTCATCAAG 451

Db 22 AAAGCCACAGCTCATCAAG 1

Query Match 0.8%; Score 18.8; DB 9; Length 51;
Best Local Similarity 90.9%; Pred. No. 1.9e+05;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 430 AAGATACAGCTCATACAAAG 451
Db 22 AAGCCACAGCTCATACAAAG 1

RESULT 86
US-10-027-805-1
Sequence 1, Application US/10027805
Patent No. US20020164725A1
GENERAL INFORMATION:

APPLICANT: ROBERTSON, Daniel E.

MURPHY, Dennis

REID, John

MAFFIA, Anthony

LINK, Steven

SMANSON, Ronald V.

WARREN, Patrick V.

KOSMOTKA, Anna

TITLE OF INVENTION: ESTERASES

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: FISH & RICHARDSON P.C.

STREET: 4225 EXECUTIVE SQUARE, STE 1400

CITY: LA JOLLA

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/027,805

FILING DATE: 21-Dec-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/602,359

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: HAITE, LISA A.

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 09010/010001

TELEPHONE: 619-678-5070

TELEFAX: 619-678-5099

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 52 NUCLEOTIDES

TYPE: NUCLEIC ACID

STRANDEDNESS: SINGLE

TOPOLOGY: LINEAR

MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-027-805-1

Query Match 0.8%; Score 18.8; DB 9; Length 52;
Best Local Similarity 68.4%; Pred. No. 1.9e+05;
Matches 26; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1734 ACACAGGAAAAATTAACGTGATTTTAAAAATCATC 1771
Db 14 AAAGAGGAGAAATTAACGTATCTTTTAAACAGCAGC 51

RESULT 87
US-09-907-900-58/c
Sequence 58, Application US/09907900

Patent No. US20020172997A1

GENERAL INFORMATION:

APPLICANT: Hartley, James L.

APPLICANT: Brasch, Michael A.

APPLICANT: Temple, Gary F.

APPLICANT: Fox, Donna K.

TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having

FILE REFERENCE: 0942.2850004

CURRENT APPLICATION NUMBER: US/09/907,900

PRIOR FILING DATE: 2001-07-19

PRIOR FILING DATE: 1998-10-23

NUMBER OF SEQ ID NOS: 60

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 58

LENGTH: 52

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: synthetic

US-09-907-900-58

Query Match 0.8%; Score 18.8; DB 9; Length 52;
Best Local Similarity 63.0%; Pred. No. 1.9e+05;
Matches 29; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 1995 TGCACCTAGGACAAATTAGCATGCAAGCTTGCTCAACTTTCCC 2040
Db 47 TACATATTGGAATGTATAGCCCTGCTTTTGTACAAACTGTGCC 2

RESULT 88

US-09-907-719-58/c

Sequence 58, Application US/09907719

Publication No. US20020192819A1

GENERAL INFORMATION:

APPLICANT: Hartley, James L.

APPLICANT: Brasch, Michael A.

APPLICANT: Temple, Gary F.

TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having

FILE REFERENCE: 0942.2850004

CURRENT APPLICATION NUMBER: US/09/907,719

PRIOR FILING DATE: 2001-07-19

PRIOR FILING DATE: 1998-10-23

NUMBER OF SEQ ID NOS: 60

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 58

LENGTH: 52

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: synthetic

US-09-907-719-58

Query Match 0.8%; Score 18.8; DB 9; Length 52;
Best Local Similarity 63.0%; Pred. No. 1.9e+05;
Matches 29; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 1995 TGCACCTAGGACAAATTAGCATGCAAGCTTGCTCAACTTTCCC 2040
Db 47 TACATATTGGAATGTATAGCCCTGCTTTTGTACAAACTGTGCC 2

RESULT 89
US-10-027-804-1
Sequence 1, Application US/10027804
Publication No. US20030054530A1

GENERAL INFORMATION:
APPLICANT: ROBERTSON, Daniel E.
MURPHY, Dennis
REID, John
MAFIA, Anthony
LINK, Steven
SWANSON, Ronald V.
WARREN, Patrick V.
KOSMOTKA, Anna
TITLE OF INVENTION: ESTERASES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON P.C.
STREET: 4225 EXECUTIVE SQUARE, STE 1400
CITY: LA JOLLA
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/027,804
FILING DATE: 21-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,359
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/010001
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5039
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 NUCLEOTIDES
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-027-804-1
Query Match 0.8%; Score 18.8; DB 9; Length 52;
Best Local Similarity 68.4%; Pred. No. 1.9e+05;
Matches 26; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 1734 ACACAGGAAAAATTAACGTGATTTTAAATCAATC 1771
DB 14 AAAGAGGAGAAATTAATGATGCTTTAAACAGCACTC 51
RESULT 90
US-09-855-797A-58/C
Sequence 58, Application US/09855797A
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Fox, Donna K.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
FILE REFERENCE: 0942, 2850008
CURRENT APPLICATION NUMBER: US/09/855,797A
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/296,281
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: US 60/065,930

PRIOR FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 58
LENGTH: 52
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-855-797A-58
Query Match 0.8%; Score 18.8; DB 10; Length 52;
Best Local Similarity 63.0%; Pred. No. 1.9e+05;
Matches 29; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 1995 TGCACTAAGACAAATTTAGCATGCAAGCTTGCTCAACTTTCCC 2040
DB 47 TACATATTGAATGATATACCTGCTTTTGTACAAACTGTGCCC 2
RESULT 91
US-09-903-410-1
Sequence 1, Application US/09903410
Patent No. US20020146799A1
GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: ROBERTSON, Dan
APPLICANT: MURPHY, Dennis
APPLICANT: REID, John
APPLICANT: MAFIA, Anthony
APPLICANT: LINK, Steven
APPLICANT: SWANSON, Ronald
APPLICANT: WARREN, Patrick
APPLICANT: KOSMOTKA, Anna
TITLE OF INVENTION: ENZYMES HAVING ESTERASE ACTIVITY AND METHODS OF USE THEREOF
FILE REFERENCE: DIVER1180-2
CURRENT APPLICATION NUMBER: US/09/903,410
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 09/382,242
PRIOR FILING DATE: 1999-08-24
PRIOR APPLICATION NUMBER: US 08/602,359
PRIOR FILING DATE: 1996-02-16
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 52
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Primer for PCR
US-09-903-410-1
Query Match 0.8%; Score 18.8; DB 10; Length 52;
Best Local Similarity 68.4%; Pred. No. 1.9e+05;
Matches 26; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 1734 ACACAGGAAAAATTAACGTGATTTTAAATCAATC 1771
DB 14 AAAGAGGAGAAATTAATGATGCTTTAAACAGCACTC 51
RESULT 92
US-09-995-225-51
Sequence 51, Application US/09995225
Publication No. US20020193584A1
GENERAL INFORMATION:
APPLICANT: Chen, Ruoping
APPLICANT: Chu, Zhi Liang
APPLICANT: Dang, Hong T.
APPLICANT: Lowitz, Kevin P.
APPLICANT: Pridle, Cameron
TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G


```
/ GENERAL INFORMATION:
/ APPLICANT: Couto, Linda B.
/ APPLICANT: Colosi, Peter C.
/ TITLE OF INVENTION: Adeno-Associated Vectors for Expression of Factor VIII
/ TITLE OF INVENTION: by Target Cells
/ FILE REFERENCE: AVigen-04082
/ CURRENT APPLICATION NUMBER: US/10/007,968
/ CURRENT FILING DATE: 2001-12-13
/ PRIOR APPLICATION NUMBER: 09/740,211
/ PRIOR FILING DATE: 2000-12-18
/ PRIOR APPLICATION NUMBER: 60/125,974
/ PRIOR FILING DATE: 1999-03-24
/ PRIOR APPLICATION NUMBER: 60/104,994
/ PRIOR FILING DATE: 1998-10-20
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 8
/ LENGTH: 59
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-007-968-8
```

```
Query Match          0.8%; Score 18.8; DB 9; Length 59;
Best Local Similarity 63.0%; Pred. No. 2.1e+05;
Matches 29; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
```

```
QY 2237 TCTTGTGAATATTAATAAATGCAATGATCATTTGTTAACAAGCT 2282
      |||||
DB 55 TATTGTTAAAGAAAGTATATTAGACGAGCTTCTGCACACAGAT 10
```

```
RESULT 100
US-10-007-280A-2
/ Sequence 2, Application US/10007280A
/ Publication No. US20030059784A1
/ GENERAL INFORMATION:
/ APPLICANT: Sun, Yongming
/ APPLICANT: Recipon, Herve
/ APPLICANT: Salceda, Susana
/ APPLICANT: Chenghua, Liu
/ TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Pro
/ FILE REFERENCE: DEX-0257
/ CURRENT APPLICATION NUMBER: US/10/007,280A
/ CURRENT FILING DATE: 2001-11-07
/ PRIOR APPLICATION NUMBER: US 60/246,640
/ PRIOR FILING DATE: 2000-11-08
/ NUMBER OF SEQ ID NOS: 238
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2
/ LENGTH: 59
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-007-280A-2
```

```
Query Match          0.8%; Score 18.8; DB 9; Length 59;
Best Local Similarity 63.0%; Pred. No. 2.1e+05;
Matches 29; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
```

```
QY 1645 AGAGGAGATGTGTGACATCTCTGCAAGTGAACAAAGACTCAAAA 1690
      |||||
DB 5 AATGTGATATGAAAGCACTACAGTATATAAACAATGCTCTCAGAA 50
```

Search completed: April 19, 2003, 12:08:13
Job time : 248 secs

LOCUS	B02929	58 bp	DNA	linear	GSS 13-JUL-1996
DEFINITION	CSRL-163B1-u CSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone CSRL-163B1, DNA sequence.				
ACCESSION	B02929				
VERSION	B02929.1	GI:1412207			
KEYWORDS	GSS.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 58) Evans G.A., Burpee D., Davies C., Hahner L., Oliver T., Gilbert M., Jones D., Ward T., Gillilan E., Schgemann J., Probst S., Harris J., Deford J., McFarland J., Buzinski K., Khan M., Kupfer K. and Garner H.R.				
TITLE	Genomic Sequence Sampled Map of Chromosome 11				
JOURNAL	Unpublished (1996)				
COMMENT	Contact: Evans GA, Shane Probst McMerritt Center for Human Growth and Development University of Texas Southwestern Medical Center At Dallas 5323 Harry Hines Blvd, Dallas TX 75235-8591 Tel: 214-648-1600 Fax: 214-648-1666 Email: g.evans@utsw.swmed.edu, shane@mcmerritt.swmed.edu Seq primer: 77 Class: cosmid ends High quality sequence stop: 58. Location/Qualifiers 1..58 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="CSRL-163B1" /clone_1ib="CSRL Flow sorted Chromosome 11 specific cosmid" /sex="female" /cell_type="chimeric hamster somatic cell hybrid" /note="Vector: scos-1; Human Chromosome 11 specific cosmid library prepared from flow sorted human Chromosome 11 derived from Chinese Hamster Ovary (CHO) monochromosomal somatic cell hybrid, J1"				
BASE COUNT	27 a	0 c	1 g	29 t	1 others
ORIGIN					
Query Match	1.1%; Score 25.2;	DB 17;	Length 58;		
Best Local Similarity	70.2%;	Pred. No. 3.8e+05;			
Matches 33;	Conservative 0;	Mismatches 14;	Indels 0;	Gaps 0;	
Cy 2106	AATCTTTTAAATAATATATATTTTCAGAAATGATTGTGATT 2152				
Db 1	AATTTATTTATTAATATATTTAGATATTTTNATAAAAAATTTTAATT 47				
RESULT 4					
LOCUS	AU269582	54 bp,	mRNA	linear	EST 10-MAY-2002
DEFINITION	AU269582 VS Dictyostelium discoideum cDNA clone VSJ214 5', mRNA sequence.				
ACCESSION	AU269582				
VERSION	AU269582.1	GI:20528380			
KEYWORDS	EST.				
SOURCE	Dictyostelium discoideum.				
ORGANISM	Dictyostelium discoideum				
REFERENCE	Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.				
AUTHORS	1 (bases 1 to 54) Urushihara H., Morio T., Saito T., Koriki F., Ochiai H., Maeda M., Takeuchi I., Kohara Y. and Tanaka Y.				
TITLE	Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum				
JOURNAL	Unpublished (2002)				
COMMENT	Contact: Hideko Urushihara Institute of Biological Sciences University of Tsukuba 1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan				

```

Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.
Location/Qualifiers
1. .54
/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSG214"
/clone_id="VS"
/sex="mat A"
/dev_stage="vegetative"
2 g 9 t

BASE COUNT 40 a 2 g 15 t
ORIGIN

Query Match 1.0%; Score 24.4; DB 9; Length 54;
Best Local Similarity 73.8%; Pred. No. 5.8e+05;
Matches 31; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Cy 1759 TAAAAATCATCATGTGTCACAAAAAACTTAAGCAAAA 1800
Db 12 TAAACCAAAAAAAAAAAGGTCACAAAAAAATTAACAAAAA 53

RESULT 5
LOCUS AU266762/c 45 bp mRNA EST 10-MAY-2002
DEFINITION AU266762 VS Dictyostelium discoideum cDNA clone VSG731 5', mRNA
sequence.
ACCESSION AU266762
VERSION AU266762.1 GI:20525560
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
REFERENCE 1 (bases 1 to 45)
AUTHORS Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
Takeuchi,I., Kohara,Y. and Tanaka,Y.
T. Population analysis of cDNAs from unicellular and multicellular
stages of Dictyostelium discoideum
Unpublished (2002)
JOURNAL Contact: Hideko Urushihara
COMMENT Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.
Location/Qualifiers
1. .45
/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSG731"
/clone_id="VS"
/sex="mat A"
/dev_stage="vegetative"
29 a 1 c 0 g 15 t
ORIGIN

Query Match 1.0%; Score 23.8; DB 9; Length 45;
Best Local Similarity 72.1%; Pred. No. 7.9e+05;
Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Cy 2110 TTTTATTAATAATATATATTTTCAAAAGATTTTGATT 2152
Db 45 TTTTATTAATAAAAAAAAAATTTAATTTATTTGTTT 3

RESULT 6
LOCUS TA261E04Q/c 42 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 261e04, reverse sequence,

```

Genomic survey sequence.

AL488612
VERSION AL488612.1 GI:11863920
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 42)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTP 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + 1 method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/
Location/Qualifiers

FEATURES
source 1..42
 /organism="Trypanosoma brucei"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="261e04"

BASE COUNT 15 a 3 c 4 g . 20 t

ORIGIN

Cy 2096 AAACAACCGATCTTTTATTATAAATATATATTTTC 2136
Db 42 AAAAAAAAAAGAAATCACTATATATATATATATATATGTTTC 2

RESULT 7
LOCUS AA761128 56 bp mRNA linear EST 07-FEB-1998
DEFINITION nz1le03.g1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287484 3',
RNA sequence.
ACCESSION AA761128
VERSION AA761128.1 GI:2810058
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 56)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
CONTACT Contact: Robert Strausberg, Ph.D.
EMAIL Email: rgsapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at www.bio.llnl.gov/bdrr/image/image.html
Insert Length: 1195 Sd Error: 0.00
Seq primer: -40m13 fwd. ET from Amer sham
High quality sequence strop: 51.

FEATURES

source

Location/Qualifiers

1..56

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1287484"

/clone_1lb="NCI_CGAP_GCB1"

/tissue_type="germinal center B cell"

/lab_host="DH10B"

/note=vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA linker; Site 1: Not I; Site 2: Eco RI; 1st strand germinal center B cells by flow sorting (CD20+, IgM-), provided by Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer

[5'-TGTTACCATCTGAAGCGAGGGCCGCCCTCAATTTTTTTTTTTT-3'] Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library was constructed through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT

18 a 2 c 7 g 29 t

ORIGIN

Query Match 1.0%; Score 23.4; DB 9; Length 56;
Best Local Similarity 73.2%; Pred. No. 9.7e+05;
Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0.

Oy 2108 TCTTTTATTATAATATATATTTTTCAAATAGATTTT 2148
|||||
4 TTTTTTTGTAGTAATAAATGAATTTTAAAAATATTTT 44

Db

RESULT 8

AA107349

LOCUS

AA107349

DEFINITION

m193a10.r1 Striatagene mouse kidney (#937315) Mus musculus cDNA clone IMAGE:519546 5' similar to SW.ATPE_MOUSE P00848 ATP SYNTHASE A CHAIN'', mRNA sequence.

ACCESSION

AA107349

KEYWORD

EST.

VERSION

AA107349.1 GI:1658632

SOURCE

house mouse.
Mus musculus.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 58)

Matta,M., Kucibler,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Hallada,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

Contact: Matta W/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LIND ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGJ:313394

Possible reversed clone: similarity on wrong strand

Seq primer: -28n13 rev1 RT from Amersham

High quality sequence stop: 1.

Location/Qualifiers

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1..56

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1287484"

/clone_1lb="NCI_CGAP_GCB1"

/tissue_type="germinal center B cell"

/lab_host="DH10B"

/note=vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA linker; Site 1: Not I; Site 2: Eco RI; 1st strand germinal center B cells by flow sorting (CD20+, IgM-), provided by Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer

[5'-TGTTACCATCTGAAGCGAGGGCCGCCCTCAATTTTTTTTTTTT-3'] Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library was constructed through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT

18 a 2 c 7 g 29 t

ORIGIN

Query Match 1.0%; Score 23.4; DB 9; Length 56;
Best Local Similarity 73.2%; Pred. No. 9.7e+05;
Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0.

Oy 2108 TCTTTTATTATAATATATATTTTTCAAATAGATTTT 2148
|||||
4 TTTTTTTGTAGTAATAAATGAATTTTAAAAATATTTT 44

Db

RESULT 8

AA107349

LOCUS

AA107349

DEFINITION

m193a10.r1 Striatagene mouse kidney (#937315) Mus musculus cDNA clone IMAGE:519546 5' similar to SW.ATPE_MOUSE P00848 ATP SYNTHASE A CHAIN'', mRNA sequence.

ACCESSION

AA107349

KEYWORD

EST.

VERSION

AA107349.1 GI:1658632

SOURCE

house mouse.
Mus musculus.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 58)

Matta,M., Kucibler,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Hallada,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

Contact: Matta W/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LIND ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGJ:313394

Possible reversed clone: similarity on wrong strand

Seq primer: -28n13 rev1 RT from Amersham

High quality sequence stop: 1.

Location/Qualifiers

```

source
1..58
/organism="Mus musculus"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:519546"
/clone_1ib="Stratagene mouse kidney (#937315)"
/sex="Females"
/tissue_type="kidney"
/dev_stage="4 weeks"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: kidney; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: 0.150 dt. Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GATTGGGACGAG 3' ~3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'"
BASE COUNT      17 a      14 c      8 g      19 t
ORIGIN

Query Match      1.0%; Score 23.4; DB 9; Length 58;
Best Local Similarity 67.3%; Pred. No. 9.7e+05;
Matches 33; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Cy 1793 AAGCAATATGATTTGCTGACTCTTAGCGACATCAATTAATGATTC 1841
      |||
Db 2 AACCAATCCATTTGGCTTATTCATTACCCACACATTAATGATTC 50

RESULT 9
BQ907332 58 bp mRNA linear EST 19-AUG-2002
LOCUS P004C10 Oryza sativa mature leaf library induced by M.grisea Oryza
BQ907332 Bativa cDNA clone P004C10, mRNA sequence.
ACCESSION BQ907332
VERSION BQ907332.1 GI:22306110
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharitoidae; Oryzaceae; Oryza.
1 (bases 1 to 58)
Dong,H.T., Li,D.B., Zhang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu
,H.F., Jiang,Y.X., Yu,P.C., Gao,Q.K. and Lou,Y.C.
A Gene Expression Screen in Oryza sativa
Unpublished (2001)
Contact: Dong HT
Laboratory of Functional Genetics
Bio-technology Institute of Zhejiang University
Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86892051
Fax: 0086-571-86961525
Email: htdong@zjuem.zju.edu.cn
Seq primer: M13 forward primer.

FEATURES
SOURCE
1..58
/organism="Oryza sativa"
/db_xref="taxon:4530"
/clone="P004C10"
/clone_1ib="Oryza sativa mature leaf library induced by
M.grisea"
/tissue_type="leaf"
/dev_stage="Mature stage"
/note="Vector: pSport2"
BASE COUNT      33 a      4 c      19 t      1 others
ORIGIN

Query Match      1.0%; Score 23.2; DB 14; Length 58;
Best Local Similarity 64.2%; Pred. No. 1.1e+06;
Matches 34; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Cy 2225 TTCGTTCTCTCTTGCGAATATATATAAAGCAATGAATCATTTGTTAA 2277
      |||
Db 55 TTTTCTTTTCTTTTAAATTAATTAATTTACTGATTAATTAATTAATTAATTA 3

```

```

RESULT 10          59 bp      DNA          linear      GSS 02-MAY-2002
BH813384
LOCUS              SALK_064078 Arabidopsis thaliana TDNA insertion lines Arabidopsis
DEFINITION        thaliana genomic clone SALK_064078, DNA sequence.
ACCESSION          BH813384
VERSION            BH813384.1  GI:20391857
KEYWORDS
ORGANISM           GSS.
SOURCE             thale cress.
Arabidopsis thaliana
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core endicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 59)
Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shim,P.,
Zimmerman,J. and Ecker,J.R.
A Sequence-indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
JOURNAL            Contact: Joseph R. Ecker
COMMENT            The Salk Institute Genomic Analysis Laboratory (SIGAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 5' end of
Atg54490.
Class: TDNA tagged.
FEATURES
Source             Location/Qualifiers
1. 59
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_064078"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/cdna\_protocols.html"
BASE COUNT        26 a 4 c 17 g 12 t
ORIGIN
Query Match       1.0%; Score 23.2; DB 17; Length 59;
Best Local Similarity 65.4%; Pred. No. 1.1e+06;
Matches 34; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
QY 2163 TGAATTCATCCCAACTTAATGCAATTTATGCTGTGGAAGATA 2214
Dbb 4 TAAATGAAGACTCAGAGCTTAATCGAATAATTAATTTGGCGGAAGAGA 55
RESULT 11
LOCUS              BG271427 50 bp mRNA linear EST 20-FEB-2001
BG271427
DEFINITION        na150f05.x1 NCI CGAP_HN20 Homo sapiens cDNA clone IMAGE:4263681 3'
mRNA sequence.
ACCESSION          BG271427
VERSION            BG271427.1  GI:12979558
KEYWORDS           EST.
SOURCE             human.
ORGANISM           Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 50)
NCI/NIH-CGAP http://www.ncbi.nlm.nih.gov/ncicg.
National Cancer Institute / National Institute of Dental Research,

```

JOURNAL
COMMENT

Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 cDNA Library Preparation: David B. Krizman, Ph.D.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL, send email to:
 info@image.lnl.gov
 Seq primer: -40UP from Glibco.
 Location/Qualifiers

FEATURES
source

1.50
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4263681"
 /clone_1lb="NCI CGAP_HN20"
 /lab_host="DH10B"
 /note="Organ: normal head/neck tissue; Vector: pAMP1; mRNA
 made from head/neck tissue, cDNA made by oligo-dT
 priming. Directionally cloned into UNG sites.
 Size-selected on agarose gel, average insert size 300 bp.
 Primary library. cDNA Library Preparation: David B.
 Krizman, Ph.D." 13 a 7 c 9 g 21 t

BASE COUNT
ORIGIN

Query Match 1.0%; Score 23; DB 12; Length 50;
 Best Local Similarity 68.1%; Pred. No. 1.2e+06;
 Matches 32; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 Cy 203 TTGGACATGACTGGCATGGAGACATTTGAGAAATTTGAATC 249
 Db 2 TTTTCTTATGACATGATTAATTTGATTCCTTACAGACTTGAATC 48

RESULT 12
 AZ508445 51 bp DNA linear GSS 05-OCT-2000
 LOCUS
 DEFINITION IM0350F1R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 ACCESSION AZ508445
 VERSION AZ508445
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 51)
 REFERENCE
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 'M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 CONTACT: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0350 row: F column: 11
 Seq primer: CACACAGGAACAGCTAGACC
 Class: plasmid ends
 High quality sequence stop: 51.
 Location/Qualifiers

1.51
 /organism="Mus musculus"
 /strain="C57BL/6J"

FEATURES
source

1.51
 /organism="Mus musculus"
 /strain="C57BL/6J"

/db_xref="taxon:10090"
 /clone="UUGC1M0350F1R"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD29, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (g14732114[9b]AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance." 11 a 4 c 0 g 36 t

BASE COUNT
ORIGIN

Query Match 1.0%; Score 23; DB 17; Length 51;
 Best Local Similarity 68.1%; Pred. No. 1.2e+06;
 Matches 32; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 Cy 2108 TCTTTTATATATATATATATATTTTCAATGATTTGATTC 2154
 Db 4 TCTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 50

RESULT 13
 AZ621827 59 bp DNA linear GSS 13-DEC-2000
 LOCUS
 DEFINITION IM0455C10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 ACCESSION AZ621827
 VERSION AZ621827
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 59)
 REFERENCE
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 'M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 CONTACT: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0455 row: C column: 10
 Seq primer: CGTTGTAAACGACGCGCACT
 Class: plasmid ends
 High quality sequence stop: 59.
 Location/Qualifiers

1.59
 /organism="Mus musculus"
 /strain="C57BL/6J"

FEATURES
source

1.59
 /organism="Mus musculus"
 /strain="C57BL/6J"

/db_xref="taxon:10090"
/clone="U9C1M0455C10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42uv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb]/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 23 a 7 c 11 g 18 t

Query Match 1.0%; Score 23; DB 17; Length 59;
Best Local Similarity 63.6%; Pred. No. 1.2e+06;
Matches 35; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 2240 TGGTGAATATATAAATGCAATGATCATTTGTTACACAGCTGTGCTGCTTTG 2294
Db 2 TTGATTAAGTATGATGACAGCAATGATGTTTACACAGCTGATCATG 56

RESULT 14
AA554929 60 bp mRNA linear EST 08-SEP-1997
LOCUS nk31905.s1 NCI CGAP Col1 Homo sapiens cDNA clone IMAGE:1015160 3'
DEFINITION similar to SW:R137_HUMAN P02403 60S RIBOSOMAL PROTEIN L37.; mRNA
sequence.
AA554929
VERSION AA554929.1 GI:2325468
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 60)
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Christopher Moskalkuk, M.D., Ph.D., Elias Campo,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/BLNt at:
www-bio.llnl.gov/bbrp/image/image.html
Insert length: 481 Std Error: 0.00
Seq primer: -40ml3 fwd. RT from Amerisham.
Location/Qualifiers
1. 60
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1015160"
/clone_lib="NCI CGAP Col1"
/tissue_type="tumor"

FEATURES
source

/lab_host="SOLR (kanamycin resistant)"
/note="Organ: colon; Vector: Bluescript SK-; Site 1: EcoRI
; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo
dr. Multiple colon tumors. 5' adaptor sequence: 5'
GAATCGGACGAG 3', 3' adaptor sequence: 5'
CTCGACTTTTCTTTTCTTTT 3' Average insert size: 1.1 kb."

BASE COUNT 10 a 3 c 2 g 45 t

Query Match 1.0%; Score 23; DB 9; Length 60;
Best Local Similarity 68.1%; Pred. No. 1.2e+06;
Matches 32; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1754 GATTTTAAAAATCAATGATGTCAGCAAAAAAATTTAAAGCAAAA 1800
Db 47 GCTTTTAAAAATTAATAAAAAAATTTAAAAAATTTAAAAA 1

RESULT 15
AM411378 60 bp mRNA linear EST 29-JUN-2000
LOCUS fh12a03.y1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2964389 3',
DEFINITION mRNA sequence.
AM411378
VERSION AM411378.1 GI:6936919
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 60)
NIH-MGC http://imgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (BLNt)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/BLNt at:
www-bio.llnl.gov/bbrp/image/image.html
Plate: LLCM64 row: B column: 6
Seq primer: M13R1 reverse primer (AB1).
Location/Qualifiers
1. 60
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2964389"
/clone_lib="NIH_MGC_17"
/tissue_type="thadomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: muscle; Vector: pOTB7; Site 1: EcoRI;
Site 2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGG(6). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 18 a 4 c 5 g 33 t

Query Match 1.0%; Score 23; DB 10; Length 60;
Best Local Similarity 68.1%; Pred. No. 1.2e+06;
Matches 32; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 2108 TCTTTTATATATATATATATTTTCAATAGATTTTGAATCA 2154
Db 12 TTTTATTTGTAAGAAAGAAATATTTATGAAACAGTTTCATTA 58

FEATURES
source

RESULT 16
 BG409218 60 bp mRNA linear EST 13-MAR-2001
 LOCUS DB88B10.Y1 Moss EST library PPG Physcomitrella patens cDNA clone
 DEFINITION PPG_SOURCE_ID:PPG_CopyA-120419.5', mRNA sequence.
 ACCESSION BG409218
 VERSION BG409218.1 GI:13315563
 KEYWORDS EST.
 SOURCE Physcomitrella patens.
 ORGANISM Physcomitrella patens
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
 1 (bases 1 to 60)
 Quattrano, R., Bashirades, S., Cove, D., Cuming, A., Knight, C., Clifton
 'S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood
 'R., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T.,
 Stepien, M., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,
 Waterston, R. and Wilson, R.
 Leeds/Mash U Moss EST Project
 Leeds/Mash U Moss EST Project
 Unpublished (1999)
 CONTACT: Ralph Quattrano
 Leeds/Mash U Moss EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 Libraries were constructed by Dr. Stavros Bashirades as part of the
 Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and
 Washington Univ. in St. Louis (USA) DNA sequencing by: Washington
 University Genome Sequencing Center For information on obtaining a
 clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)
 Putative full length read
 vector to vector length is 61
 Seq primer: -40RP from GIBCO.
 Location/Qualifiers
 1. 60
 /organism="Physcomitrella patens"
 /db_xref="taxon:3218"
 /clone="PEP_SOURCE_ID:PPG_CopyA-120419"
 /clone_1b="Moss EST library PPG"
 /tissue_type="gametophore: 30 day old tissue,
 ammonium-grown"
 /lab_host="DH10B"
 /note="Vector: PAMPI; Construction of the cDNA library was
 performed by Dr. W. Gregg Clark using a modification of
 the cDNA synthesis protocol developed in the laboratory of
 Dr. Michael Lovett by Dr. Yulia Korshunova (personal
 communication). First polyA + RNA was isolated from total
 gametophore RNA using oligo dt magnetic beads. Following
 this, first strand cDNA synthesis was performed on the
 bead-bound polyA + RNA, during which an oligonucleotide
 anchor sequence was incorporated onto the 5'-ends of the
 cDNA. PCR amplification was then used to synthesize the
 second strand, to amplify the double stranded DNA, and to
 incorporate dUTP containing sequences into the ends of the
 double stranded cDNA. This DNA was size selected and
 cloned into PAMPI using the CloneAMP PAMPI System (Life
 Technologies, GibcoBRL) for cloning amplification products
 by a non-restriction site dependent process. The cloning
 was directional based on sequence asymmetry introduced at
 the ends during PCR amplification. The 3' cDNA ends are
 proximal to the NotI site of the multiple cloning site in
 PAMPI. This annealing mixture was transformed into
 chemically competent DH10B cells and selected for
 ampicillin resistant growth. The resulting clones (about
 330,000) were pooled to make the library."

Matches 32; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 QY 1742 AAGATAACGTGATTTTAAATAATCATCATGTCGCAAAAAA 1788
 Db 14 AAGCTAAGTAGTAGTAGTAGTAGTAATAATAATAGTAAAAA 60

RESULT 17
 AM249993 52 bp mRNA linear EST 07-JAN-2000
 LOCUS AM249993/c
 DEFINITION 2819345.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819345.3',
 mRNA sequence.
 ACCESSION AM249993
 VERSION AM249993.1 GI:6592986
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 52)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Other_ESTs: 2819345.3prime
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: DCTD/DPF cDNA Library Preparation: Ling
 Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
 Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing
 Project Clone distribution: MGC clone distribution information can
 be found through the I.M.A.G.E. Consortium/LNL at:
 www-bio.1lnl.gov/db/ftp/image/image.html Base Calling / Quality
 Scores: PHRED from University of Washington Genome Center
 Trimming: cross match from University of Washington Genome Center
 PHRAP suite. Poly-T identification: patmatch.pl from Berkeley
 Drosophila Genome Project. University of Washington Genome Center:
 http://www.genome.washington.edu Low Quality Sequence: 8 contiguous
 PHRED high quality bases following vector sequence. Very low
 Quality Sequence: Trace file contained 52 contiguous distinct peaks
 following vector sequence. Polyadenylation: Based upon the presence
 of a XhoI site followed by a run of 14 or more T residues at the
 beginning of the sequence, this cDNA insert was polyadenylated.
 Plate: LCM1 row: F column: 18
 High quality sequence stop: 8.
 Location/Qualifiers
 1. 52
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2819345"
 /clone_1b="NIH_MGC_7"
 /tissue_type="small cell carcinoma"
 /cell_line="MG3"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: lung; Vector: POTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAAGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

FEATURES

source
 1. 52
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2819345"
 /clone_1b="NIH_MGC_7"
 /tissue_type="small cell carcinoma"
 /cell_line="MG3"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: lung; Vector: POTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAAGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 BASE COUNT 7 a 3 c 6 g 36 t
 ORIGIN

Query Match 1.0%; Score 22.8; DB 10; Length 52;
 Best Local Similarity 66.0%; Pred. No. 1.3e+06;
 Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1738 AGGAAATTAAGTGAATTTTAAATAATCATCATGTCGCAAAAAA 1787
 Db 50 AGGAAATTAAGTGAATTTTAAATAATCATCATGTCGCAAAAAA 1

BASE COUNT 34 a 2 c 11 g 13 t
 ORIGIN
 Query Match 1.0%; Score 23; DB 12; Length 60;
 Best Local Similarity 68.1%; Pred. No. 1.2e+06;

RESULT 18
LOCUS BM880091/c
DEFINITION ku0402.v1 Strongyloides ratii PA female naive pAMP1 v1
ACCESSION BM880091
VERSION BM880091.1 GI:19252758
KEYWORDS EST
SOURCE Strongyloides ratii
ORGANISM Strongyloides ratii
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Panagrolaimidae; Strongyloidae; Strongyloides.
REFERENCE 1 (bases 1 to 53)
McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T., Darke,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Taggarajshvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., Peterson,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
COMMENT The Washington Univ. Nematode EST Project, 1999
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Brandi Chiapelli and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dyna1). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. Dissected nematode tissues were provided by Dr. Alan Scott (ascott@hshp.edu) of the School of Public Hygiene and Public Health at John Hopkins University in Baltimore, MD.
LOCATION/Qualifiers
1. 53
/organism="Strongyloides ratii"
/db_xref="taxon:34506"
/clone_lib="Strongyloides ratii PA female naive pAMP1 v1"
/dev_stage="Parasitic adult females"
/lab_host="DH10B"
/note="Vector: PAMP1 (Gibco); Site 1: NotI; Site 2: SalI; Chiapelli and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dyna1). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. Parasitic adult females were collected from naive animals and provided by Dr. Mark Viney of Bristol, UK."

BASE COUNT 36 a 2 c 2 g 13 t
ORIGIN

Query Match 1.0%; Score 22.8; DB 14; Length 53;
Best Local Similarity 71.4%; Pred. No. 1.3e+06;
Matches 30; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 2108 TCTTTTATATATATATATATATATATATATATATATATG 2149
Db 47 TTTTATATATATATATATATATATATATATATATATATG 6

RESULT 19
LOCUS AZ482068/c
DEFINITION 54 bp DNA linear GSS 04-OCT-2000
c10ne UGCG1M0306M23 R, DNA sequence.
ACCESSION AZ482068
VERSION AZ482068.1 GI:10643133
KEYWORDS GSS.

SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 54)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Kelly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0306 row: M column: 23
Seq primer: CACACAGAAACGCTATGACC
Clase: plasmid ends
High quality sequence stop: 54.
LOCATION/Qualifiers
1. 54
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="UGCG1M0306M23"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/sex="Male"
/lab_host="E. Coli strain XJ10-Gold, T1-resistant, F-"
/note="Vector: PMD42n; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (GI:4732114|9D|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XJ10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 31 a 4 c 9 g 10 t
ORIGIN

Query Match 1.0%; Score 22.8; DB 17; Length 54;
Best Local Similarity 71.4%; Pred. No. 1.3e+06;
Matches 30; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 2094 GCAACACCTGATCTTTTATATATATATATATATATAT 2135
Db 42 GCAACACCTGATCTTTTATATATATATATATATATAT 1

RESULT 20
LOCUS AU264598/c
DEFINITION 59 bp mRNA linear EST 10-MAY-2002
AU264598 VS Dictyostelium discoideum cDNA clone VSD814.5', mRNA
sequence.
ACCESSION AU264598
VERSION AU264598.1 GI:20523396
KEYWORDS EST.

SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum
REFERENCE Eukaryota; Mycetozoa; Dictyostelid; Dictyostelium.
AUTHORS 1 (bases 1 to 59)
TITLE Urushihara, H., Morio, T., Saito, T., Koriki, E., Ochiai, H., Maeda, M.,
Takeuchi, I., Kohara, Y. and Tanaka, Y.
Population analysis of cDNAs from unicellular and multicellular
stages of Dictyostelium discoideum
JOURNAL Unpublished (2002)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.

FEATURES
source
1. 59
/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSD814"
/sex="mat A"
/dev_stage="vegetative"

BASE COUNT 30 a 4 c 1 g 24 t

ORIGIN

Query Match 1.0%; Score 22.8; DB 9; Length 59;
Best Local Similarity 62.1%; Pred. No. 1.3e+06;
Matches 36; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 2110 TTTTATTAATATATATATTTTCAATAGATTTTGATTCAGCTCATTAAGAA 2167
Db 59 TTTTATTAATTAAGTAACTTAATTAATCAATGTTTAAATTTGATTAAGAA 2

RESULT 21
AU26778/c 59 bp mRNA linear EST 10-MAY-2002
LOCUS AU267788 VS Dictyostelium discoideum cDNA clone VSH663 5', mRNA
DEFINITION
SEQUENCE AU267788
VERSION AU267788.1 GI:20526586
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Eukaryota; Mycetozoa; Dictyostelid; Dictyostelium.
REFERENCE 1 (bases 1 to 59)
AUTHORS Urushihara, H., Morio, T., Saito, T., Koriki, E., Ochiai, H., Maeda, M.,
Takeuchi, I., Kohara, Y. and Tanaka, Y.
Population analysis of cDNAs from unicellular and multicellular
stages of Dictyostelium discoideum
JOURNAL Unpublished (2002)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.

FEATURES
source
1. 59
/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSH663"
/clone_1lb="VS"
/sex="mat A"
/dev_stage="vegetative"

BASE COUNT 30 a 4 c 1 g 24 t

ORIGIN

Query Match 1.0%; Score 22.8; DB 9; Length 59;
Best Local Similarity 62.1%; Pred. No. 1.3e+06;
Matches 36; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 2110 TTTTATTAATATATATATTTTCAATAGATTTTGATTCAGCTCATTAAGAA 2167
Db 59 TTTTATTAATTAAGTAACTTAATTAATCAATGTTTAAATTTGATTAAGAA 2

RESULT 22
BQ397088/c 59 bp mRNA linear EST 22-MAY-2002
LOCUS BQ397088
DEFINITION NISC_ng25f10.x1 NICHD XGC Emb6 Silurana tropicalis cDNA clone
IMAGE:5384586 3', mRNA sequence.
ACCESSION BQ397088
VERSION BQ397088.1 GI:21084775
KEYWORDS EST.
SOURCE western clawed frog.
ORGANISM Silurana tropicalis
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Silurana.
REFERENCE 1 (bases 1 to 59)
AUTHORS NIH-XGC http://image.llnl.gov/image/html/xenopuslib.info.shtml.
TITLE National Institute of Child Health and Human Development, National
Cancer Institute, Xenopus Gene Collection
JOURNAL Unpublished (2002)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@b6-remail.nih.gov
CNA Library Preparation:
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
Plate: LLM11979 row: K column: 19
Seq primer: -21M13 forward primer (ABI).
Location/Qualifiers
1. 59
/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="IMAGE:5384586"
/clone_1lb="NICHD XGC Emb6"
/tissue_type="neural"
/dev_stage="embryo, stages 14-19"
/lab_host="DH10B (phage-resistant)"
/note="vector: PCWV-SPORE.cdb, Site1: NotI, Site2:
EcoRV; Cloned unidirectionally. Primer: Oligo dT. Average
insert size 2.1 kb. Constructed by invitrogen. Note: This
is a Xenopus Gene Collection (XGC) library."

BASE COUNT 2 a 2 c 1 g 54 t

ORIGIN

Query Match 1.0%; Score 22.8; DB 14; Length 59;
Best Local Similarity 62.1%; Pred. No. 1.3e+06;
Matches 36; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 1743 AAATAACGCGATTTAAATATCAATGTCGAAAAAACTTAAGCAAA 1800
Db 59 AAAAAACAAAAAGTAAAAATAAAAATAAAAATAAAAATAAAAATAAAA 2

RESULT 23
AU266759/c 51 bp mRNA linear EST 10-MAY-2002
LOCUS AU266759 VS Dictyostelium discoideum cDNA clone VSG728 5', mRNA
DEFINITION
SEQUENCE AU266759
VERSION AU266759.1 GI:20525557
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum

REFERENCE	Eukaryota; Mycetozoa; Dictyostelidia; Dictyostelium.
AUTHORS	1 (bases 1 to 51)
TITLE	Urushihara, H., Morio, T., Saito, T., Korihi, E., Ochiai, H., Maeda, M., Takeuchi, I., Kohara, Y. and Tanaka, Y.
JOURNAL	Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum.
COMMENT	Unpublished (2002)
FEATURES	Contact: Hideko Urushihara Institute of Biological Sciences University of Tsukuba 1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan Tel: 81-298-53-4664 Fax: 81-298-53-6614 Email: hideko@biol.tsukuba.ac.jp. Location/Qualifiers
SOURCE	1. 51 /organism="Dictyostelium discoideum" /strain="AX4" /db_xref="taxon:44689" /clone="VSG728" /clone_1ib="VS" /sex="mat A" /dev_stage="vegetative"
BASE COUNT	30 a 3 c 3 g 15 t
ORIGIN	
Query Match	1.0%; Score 22.6; DB 9; Length 51;
Best Local Similarity	68.9%; Pred. No. 1.5e+06;
Matches	31; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Oy	2108 TCTTTTATTAATAATATATTTTCAATAGATTTTCAAT 2152
Db	49 TTTTTCATATTTAAATATATATATATCAAAATTTATTTGATT 5
RESULT 24	
AU006675/c	
LOCUS	AU006675 53 bp mRNA EST 31-JUL-1998
DEFINITION	AU006675 Schizosaccharomyces pombe late log phase cDNA
ACCESSION	Schizosaccharomyces pombe cDNA clone spc00272, mRNA sequence.
VERSION	AU006675
KEYWORDS	AU006675.1 GI:343134
SOURCE	EST.
ORGANISM	Fission yeast.
COMMENT	Schizosaccharomyces pombe Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomycetes. 1 (bases 1 to 53) Moriyomo, M. and Mita, K. Moriyomo, M. and Mita, K. Identification of expressed sequence tags of Schizosaccharomyces pombe Unpublished (1998) Contact: Mitsunori Moriyomo Genome Research Group National Institute of Radiological Sciences 9-1, Anagawa-4-chome, Inage-Ku, Chiba, Chiba 263-8555, Japan Email: moriyomo@nirs.go.jp. Location/Qualifiers
JOURNAL	
COMMENT	
FEATURES	1. 53 /organism="Schizosaccharomyces pombe" /strain="972" /db_xref="taxon:4896" /clone="spc00272" /clone_1ib="Schizosaccharomyces pombe late log phase cDNA" /sex="h minus" /note="Vector: M13mp19. The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"
BASE COUNT	23 a 6 c 5 g 19 t

```

ORIGIN
Query Match      1.0%; Score 22.6; DB 9; Length 53;
Best Local Similarity 75.7%; Pred. No. 1.5e+06;
Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2110 TTTTATTAATTAATATATATATTTTCAATGAAATTT 2146
      ||||| ||| ||| ||| ||| ||| ||| ||| |||
DB 53 TTTTATTAATGATATAGGCTTTTCAAAATTCATTT 17

RESULT 25
AU264938 56 bp mRNA linear EST_10-MAY-2002
AU264938 VS Dictyostelium discoidium cDNA clone VSP251 5', mRNA
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
Takahashi, I., Kohara, Y. and Tanaka, Y.,
Population analysis of cDNAs from unicellular and multicellular
stages of Dictyostelium discoidium
Unpublished (2002)
Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.

FEATURES
Source
location/Qualifiers
1..56
/organism="Dictyostelium discoidium"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSP251"
/clone_lib="VS"
/sex="mat A"
/dev_stage="vegetative"
2..16 c 16 t 2 others

BASE COUNT 36 a 2 c 0 g 16 t 2 others
ORIGIN

Query Match      1.0%; Score 22.6; DB 9; Length 56;
Best Local Similarity 66.0%; Pred. No. 1.5e+06;
Matches 31; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1742 AAAATTAACGTGATTTTAAACAAATCATCATGATGCAAAAAA 1788
      ||||| ||| ||| ||| ||| ||| ||| ||| |||
DB 8 AAAATTAACAAATTTTAAATTAACAAACAAATTTTAAACAAAAA 54

RESULT 26
B03428 56 bp DNA linear GSS 13-JUL-1996
DEFINITION
CSRL-17998-u CSRL flow sorted chromosome 11 specific cosmid Homo
sapiens genomic clone CSRL-17998, DNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 56)
Evans, G.A., Burpee, D., Davies, C., Hahner, L., Oliver, T., Gilbert, M.,
Jones, D., Ward, T., Gillilan, E., Schagemann, J., Probst, S., Harris,
D., Deford, J., McFarland, J., Burzinski, K., Khan, M., Kupfer, K. and
Gartner, H. R.

```

TITLE
JOURNAL
COMMENT

Genomic Sequence Sampled Map of Chromosome 11
Unpublished (1996)
Contact: Evans GA, Shane Probst
McDermott Center for Human Growth and Development
University of Texas Southwestern Medical Center At Dallas
5323 Harry Hines Blvd, Dallas TX 75235-8591
Tel: 214-648-1600
Fax: 214-648-1666
Email: gevas@utsw.swmed.edu, shane@mcdermott.swmed.edu
Seq primer: T7
Class: cosmid ends
High quality sequence stop: 56.
Location/Qualifiers

FEATURES
source

1..56
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSRL-179A8"
/clone_1lb="CSRL flow sorted Chromosome 11 specific cosmid"
/sex="female"
/cell_type="chimeric hamster somatic cell hybrid"
/note="Vector: sCos-1; Human Chromosome 11 specific cosmid library prepared from flow sorted human Chromosome 11 derived from Chinese Hamster Ovary (CHO) monochromosomal somatic cell hybrid, J1"
24 a 4 c 1 g 26 t 1 others
Query Match 1.0%; Score 22.6; DB 17; Length 56;
Best Local Similarity 73.7%; Pred. No. 1.5e+06;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

BASE COUNT
ORIGIN

2115 TTATATATATATATATATTTCAATAGATTTTGATT 2152
Db 17 TTAATAATAAATTTTATTTTAAATTTTAAATT 54

RESULT 27
LOCUS AA815875 57 bp mRNA linear EST 13-FEB-1998
DEFINITION v774b01.1 Knowles Solter mouse blastocyst B3 Mus musculus cDNA.
clone IMAGE:1082377 5', mRNA sequence.
ACCESSION AA815875
VERSION AA815875.1 GI:2865471
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 57)
Marras, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
The WashU-HMNI Mouse EST Project
Unpublished (1996)
Contact: Marras M/Mouse EST Project
WashU-HMNI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LINT; contact the IMAGE Consortium (info@image.lim.gov) for further information.
MGI:596673.

FEATURES
source

1..57
/organism="Mus musculus"
/strain="C57BL/6J x DBA/2J F1"
/db_xref="taxon:10090"
/clone="IMAGE:1082377"

/clone_1lb="Knowles Solter mouse blastocyst B3"
/tissue_type="blastocyst"
/dev_stage="embryo (pre-implantation)"
/lab_host="DH10B"
/note="Organ: embryo; Vector: pSPORT; Site 1: NotI; Site 2: SalI; Cloned unidirectionally from mRNA prepared from 800 Blastocysts. Primer: SalI(dT). CDNAs were 5'-CGGTGACCGTCGACCGCTTTTCTTTT-3'. CDNAs were cloned into the NotI/SalI sites of a pSPORT vector (Life Technologies). Two different size selections: B1 (larger inserts) and B3."
50 a 4 c 1 g 2 t
Query Match 1.0%; Score 22.6; DB 9; Length 57;
Best Local Similarity 68.9%; Pred. No. 1.5e+06;
Matches 31; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

BASE COUNT
ORIGIN

2108 TCTTTTATATATATATATATTTTCAATAGATTTTGATT 2152
Db 53 TTTTATATATATATATATTTTCAATAGTTGTTTGT 9

RESULT 28
LOCUS B00931 58 bp DNA linear GSS 13-JUL-1996
DEFINITION CSRL-122a1-u CSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone CSRL-122a1, DNA sequence.
ACCESSION B00931
VERSION B00931.1 GI:1410209
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 58)
Evans, G.A., Burbee, D., Davies, C., Hahner, L., Oliver, T., Gilbert, M., Jones, D., Ward, T., Gillilan, E., Schlegelman, J., Probst, S., Harris, J., Deford, J., McFarland, J., Burzinski, K., Khan, M., Kupfer, K. and Garner, H.R.
Genomic Sequence Sampled Map of Chromosome 11
Unpublished (1996)
Contact: Evans GA, Shane Probst
McDermott Center for Human Growth and Development
University of Texas Southwestern Medical Center At Dallas
5323 Harry Hines Blvd, Dallas TX 75235-8591
Tel: 214-648-1600
Fax: 214-648-1666
Email: gevas@utsw.swmed.edu, shane@mcdermott.swmed.edu
Seq primer: T7
Class: cosmid ends
High quality sequence stop: 58.
Location/Qualifiers

FEATURES
source

1..58
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSRL-122a1"
/clone_1lb="CSRL flow sorted Chromosome 11 specific cosmid"
/sex="female"
/cell_type="chimeric hamster somatic cell hybrid"
/note="Vector: sCos-1; Human Chromosome 11 specific cosmid library prepared from flow sorted human Chromosome 11 derived from Chinese Hamster Ovary (CHO) monochromosomal somatic cell hybrid, J1"
30 a 3 c 5 g 19 t 1 others
Query Match 1.0%; Score 22.6; DB 17; Length 58;
Best Local Similarity 67.4%; Pred. No. 1.5e+06;
Matches 31; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

BASE COUNT
ORIGIN

2096 AACCACTGAATCTTTTATATATATATATATTTTCAATA 2141

Db 5 ANAAAAAAAAAGTTTATATATAAATTAATTTTATATAA 50

RESULT 29

LOCUS CDS06CC9 60 bp DNA linear GSS 17-JUN-2001

DEFINITION T3 end of clone AROAA003G11 of library AROAA from strain CBS 732 of *Zygosaccharomyces rouxii*, genomic survey sequence.

ACCESSION AL392335

VERSION AL392335.1 GI:12141583

KEYWORDS GSS.

SOURCE *Zygosaccharomyces rouxii*.

ORGANISM *Zygosaccharomyces rouxii*.

REFERENCE 1 (bases 1 to 60)

AUTHORS Souciet, J., Aigle, M., Attiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, B., Broctier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durand, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuvéglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissbach, J.

TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies

JOURNAL FEBS Lett. 487 (1), 3-12 (2000)

MEDLINE 20584711

PUBMED 1152876

REFERENCE 2 (bases 1 to 60)

AUTHORS de Montigny, J., Straub, M., Potier, S., Tekala, F., Dujon, B., Wincker, P., Attiguenave, F. and Souciet, J.

TITLE Genomic exploration of the hemiascomycetous yeasts: 8. *Zygosaccharomyces rouxii*

JOURNAL FEBS Lett. 487 (1), 52-55 (2000)

MEDLINE 20584718

PUBMED 1152883

REFERENCE 3 (bases 1 to 60)

AUTHORS Genoscope.

TITLE Direct Submission

COMMENT Submitted (06-SEP-2000) Genoscope - Centre National de Séquençage, 2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqret@genoscope.cns.fr - Web: www.genoscope.cns.fr)

REFERENCE 4 (bases 1 to 60)

AUTHORS This GSS is part of a random genomic sequencing program of thirteen yeast species: *Saccharomyces bayanus* var. *uvatum*, *Saccharomyces exiguus*, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*, *Saccharomyces kluyveri*, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

source 1.60

Location/Qualifiers

1.60

/organism="Zygosaccharomyces rouxii"

/strain="CBS 732"

/db_xref="taxon:4956"

/clone="AROAA003G11"

/clone_id="AROAA"

/note="end: T3"

BASE COUNT 5 a 1 c 0 g 53 t 1 others

ORIGIN

Query Match 1.0%; Score 22.6; DB 17; Length 60;

Best Local Similarity 66.0%; Pred. No. 1.5e+06;

Matches 31; Conservative 1; Mismatches 15; Indels 0; Gaps 0;

Qy 2106 AATCTTTTATATAATATATATTTTCAATAGATTTTGATT 2152

Db 10 AATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 56

RESULT 30

AU265345/c

LOCUS AU265345 59 bp mRNA linear EST 10-MAY-2002

DEFINITION AU265345 VS *Dictyostelium discoideum* cDNA clone VSF512 5', mRNA sequence.

ACCESSION AU265345

VERSION AU265345.1 GI:20524143

KEYWORDS EST.

SOURCE *Dictyostelium discoideum*.

ORGANISM *Dictyostelium discoideum*.

REFERENCE 1 (bases 1 to 59)

AUTHORS Urushihara, H., Morio, T., Saito, T., Koriki, E., Ochiai, H., Maeda, M., Takeuchi, I., Kohara, Y. and Tanaka, Y.

TITLE Population analysis of cDNAs from unicellular and multicellular stages of *Dictyostelium discoideum*

JOURNAL Unpublished (2002)

COMMENT Contact: Hideko Urushihara

Institute of Biological Sciences

University of Tsukuba

1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan

Tel: 81-298-53-4664

Fax: 81-298-53-6614

Email: hideko@biol.tsukuba.ac.jp.

FEATURES

source 1.60

Location/Qualifiers

1.60

/organism="Dictyostelium discoideum"

/strain="AX4"

/db_xref="taxon:44689"

/clone="VSF512"

/clone_id="VS"

/sex="mat A"

/dev_stage="vegetative"

BASE COUNT 30 a 0 c 4 g 17 t 8 others

ORIGIN

Query Match 1.0%; Score 22.4; DB 9; Length 59;

Best Local Similarity 57.1%; Pred. No. 1.6e+06;

Matches 32; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 2080 TTGATGTTTACGCGCAACACCTGATCTTTTATATATATATATTTT 2155

Db 59 TTTTATTTTAAANNNAANCCCAATTTTATTTTAAANNNAATTTT 4

RESULT 31

LOCUS AU263817 60 bp mRNA linear EST 10-MAY-2002

DEFINITION AU263817 VS *Dictyostelium discoideum* cDNA clone VSD310 3', mRNA sequence.

ACCESSION AU263817

VERSION AU263817.1 GI:20522615

KEYWORDS EST.

SOURCE *Dictyostelium discoideum*.

ORGANISM *Dictyostelium discoideum*.

REFERENCE 1 (bases 1 to 60)

AUTHORS Urushihara, H., Morio, T., Saito, T., Koriki, E., Ochiai, H., Maeda, M., Takeuchi, I., Kohara, Y. and Tanaka, Y.

TITLE Population analysis of cDNAs from unicellular and multicellular stages of *Dictyostelium discoideum*

JOURNAL Unpublished (2002)

COMMENT Contact: Hideko Urushihara

Institute of Biological Sciences

University of Tsukuba

1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan

Tel: 81-298-53-4664

Fax: 81-298-53-6614

Email: hideko@biol.tsukuba.ac.jp.

FEATURES

source 1.60

Location/Qualifiers

1.60

/organism="Dictyostelium discoideum"

/strain="AX4"

/db_xref="taxon:44689"

	BASE COUNT	23 a	3 c	1 g	22 t	11 others
ORIGIN						
Query Match	1.0%	Score 22.4;	DB 9;	Length 60;		
Best Local Similarity	54.2%	Pred. No.1.6e+06;				
Matches 32; Conservative	0;	Mismatches 27;	Indels 0;	Gaps 0;		
Oy	2062	ACAAAGAACTTACCATTGATGTGTTTACCGCAACAACCTGAATCTTTTTTATA	2120			
Dn	1	AAAAAAAAAATACAAATTGTTGTTNTTTTTTTTTTNAAAAAACNNANNNTNNTTTNAAA	59			
RESULT 32	AU268768	44 bp	mRNA	linear	EST 10-MAY-2002	
AU268768/c						
LOCUS	AU268768	VS Dictyostelium discoideum cdna clone VS1483 5'				
DEFINITION						
sequence.						
ACCESSION	AU268768					
VERSION	AU268768.1	GI:20527566				
KEYWORDS	EST.					
SOURCE	Dictyostelium discoideum.					
ORGANISM	Dictyostelium discoideum.					
REFERENCE	Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.					
AUTHORS	1 (bases 1 to 44)					
TITLE	Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M., Takeuchi,I., Kohara,Y. and Tanaka,Y. Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum Unpublished (2002)					
JOURNAL	Contact: Hideko Urushihara Institute of Biological Sciences University of Tsukuba 1-1-1 Tenoudai, Tsukuba, Ibaraki 305-8572, Japan Tel: 81-298-53-4664 Fax: 81-298-53-6614 Email: hideko@biol.tsukuba.ac.jp.					
COMMENT	Location/Qualifiers					
FEATURES	1..44					
source	/organism="Dictyostelium discoideum" /strain="AX4" /db_xref="taxon:44689" /clone="VS1483" /clone_lib="VS" /sex="mat A" /dev_stage="vegetative"					
	BASE COUNT	30 a	0 c	0 g	14 t	
ORIGIN						
Query Match	0.9%	Score 22.2;	DB 9;	Length 44;		
Best Local Similarity	69.8%	Pred. No.1.8e+06;				
Matches 30; Conservative	0;	Mismatches 13;	Indels 0;	Gaps 0;		
Oy	2108	TCCTTTTTTATATTAATATATATATTTTCCAAATAGATTTTGCA	2150			
Dn	43	TTTTTTTTTAATATATATATATATTTAAATATATTTATTTTA	1			
RESULT 33	AU268819	44 bp	mRNA	linear	EST 10-MAY-2002	
AU268819/c						
LOCUS	AU268819	VS Dictyostelium discoideum cdna clone VS1519 3'				
DEFINITION						
sequence.						
ACCESSION	AU268819	GI:20527617				
VERSION	AU268819.1					
KEYWORDS	EST.					
SOURCE	Dictyostelium discoideum.					
ORGANISM	Dictyostelium discoideum.					
REFERENCE	Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.					
	1 (bases 1 to 44)					

AUTHORS	Urushihara,H., Morio,T., Saito,T., Kozaki,E., Ochiai,H., Maeda,M., Takenuchi,I., Kohara,Y. and Tanaka,Y.			
TITLE	Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum			
JOURNAL	Unpublished (2002)			
COMMENT	Contact: Hideko Urushihara Institute of Biological Sciences University of Tsukuba 1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan Tel: 81-298-53-4664 Fax: 81-298-53-6614 Email: hideko@biol.tsukuba.ac.jp.			
FEATURES	Location/Qualifiers			
SOURCE	1..44			
	/organism="Dictyostelium discoideum"			
	/strain="AX4"			
	/db_xref="taxon:44689"			
	/clone="VS1519"			
	/clone_1lb="VS"			
	/sex="mat A"			
	/dev_stage="vegetative"			
BASE COUNT	30	a	2 c	1 g 10 t 1 others
ORIGIN				
Query Match	0.9%; Score 22.2; DB 9; Length 44;			
Best Local Similarity	68.2%; Pred. No. 1.8e+06;			
Matches	30;	Conservative	0;	Mismatches 14; Indels 0; Gaps 0;
QY	2104	TGAACTCTTTTATATATATATATATTTTCAATGATTTT 2147		
DB	44	TAATTTTATTTTATTTTATTTTATTTTATTTTAACTAGAGTTT 1		
RESULT 34				
LOCUS	BF643229 52 bp mRNA linear EST 20-DEC-2000			
DEFINITION	NF0020808C1F1062 Elicted cell culture Medicago truncatula cDNA			
ACCESSION	BF643229			
VERSION	BF643229.1 GI:11908354			
KEYWORDS	EST.			
SOURCE	barrel medic.			
ORGANISM	Medicago truncatula			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons, core eudicots; Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.			
REFERENCE	1 (bases 1 to 52) Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation - Center for Medicago Genomics Research Unpublished (2000)			
AUTHORS	Contact: Dixon RA Plant Biology Division The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7302 Fax: 580 221 7380 Email: radixon@noble.org			
JOURNAL	Insert Length: 52 Std Error: 0.00 Plate: 002 row: B column: 08			
COMMENT	Seq primer: TCACACAGGAAACGCTATGAC. Location/Qualifiers			
FEATURES	1..52			
SOURCE	/organism="Medicago truncatula"			
	/db_xref="taxon:3880"			
	/clone="NF002B08EC"			
	/clone_1lb="Elicted cell culture"			
	/tissue_type="Cell cultures derived from root tissues"			
	/dev_stage="Cell suspensions were subcultured every 14 days. Cells were induced six days after subculture"			
	/note="Vector: Lambda Zap; Cells were induced with yeast			

REFERENCE
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 58)
JOURNAL Gubin,A.N., Njoroge,J.M., Bouffard,G.G. and Miller,J.L.
MEDLINE Gene expression in proliferating human erythroid cells
 Genomics 59 (2), 168-177 (1999)
 99339981

COMMENT
 Contact: Jeffery L. Miller
 Laboratory of Chemical Biology
 National Institute of Diabetes and Digestive and Kidney Diseases
 Building 10, Room 9B17, National Institutes of Health, Bethesda, MD
 20892, USA
 Tel: 301 402 2373
 Fax: 301 435 5148
 Email: jm7f@nih.gov
FEATURES
 DNA Sequencing and analyses by National Institutes of Health
 Intramural Sequencing Center (NISC).
 Plate: 38 row: e column: 11
 Seq primer: -21M13 forward primer (ABI).
 Location/Qualifiers
 1..58
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="ax38e11"
 /clone_1b="Proliferating Human Erythroid Cells (LCB:ax
 library)"
 /sex="unknown"
 /tissue_type="blood"
 /cell_type="Erythroid Cells"
 /cell_line="Primary Culture of Peripheral Blood
 Mononuclear Cells"
 /dev_stage="Progenitor; EPO responsive CD71++++"
 /lab_host="SOLR"
 /note="Organ: blood; Vector: Lambda ZAP II; Site 1: EcoRI;
 Site 2: EcoRI; 65,000 proliferating erythroid cells from
 the buffy coat of a blood donation were obtained by flow
 cytometric separation after a 5-day culture period in the
 presence of erythropoietin. Total RNA was purified from
 the sorted cell population using RNeasy reagent. RNA (0.3
 ug) was converted into double stranded cDNA using
 Clontech's Capfinder cDNA Library Construction Kit
 (Clontech) according to the manufacturer's protocol and
 cloned into EcoRI digested Lambda Zap II vector
 (Stratagene). The phage library was amplified once prior
 to in vivo excision in SOLR cells. Individual colonies
 were grown, and the cDNA inserts were sequenced in high
 throughput (NIH Intramural Sequencing Center
 http://www.nisc.nih.gov/)."

BASE COUNT
 0 a 6 c 2 g 50 t

ORIGIN

Query Match 0.9%; Score 22.2; DB 13; Length 58;
Best Local Similarity 69.8%; Pred. No. 1.8e+06;
Matches 30; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1760 AAAAAATCAATGTCGCAAAAAAAGCTTAAGCAAAATA 1802
 Db 47 AAAAAAAAAAAAAAAAAAGAAAAAAGAAAAAAGAAAAA 5

RESULT 41
LOCUS BG943837/c 59 bp mRNA linear EST 11-JUN-2001
DEFINITION ax42f06.x1 Proliferating Human Erythroid Cells (LCB:ax library)
ACCESSION BG943837
VERSION BG943837.1 GI:14343209
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 59)
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Gubin,A.N., Njoroge,J.M., Bouffard,G.G. and Miller,J.L.
TITLE Gene expression in proliferating human erythroid cells
JOURNAL Genomics 59 (2), 168-177 (1999)
MEDLINE 99339981

COMMENT
 Contact: Jeffery L. Miller
 Laboratory of Chemical Biology
 National Institute of Diabetes and Digestive and Kidney Diseases
 Building 10, Room 9B17, National Institutes of Health, Bethesda, MD
 20892, USA
 Tel: 301 402 2373
 Fax: 301 435 5148
 Email: jm7f@nih.gov
FEATURES
 DNA Sequencing and analyses by National Institutes of Health
 Intramural Sequencing Center (NISC).
 Plate: 42 row: f column: 06
 Seq primer: -21M13 forward primer (ABI).
 Location/Qualifiers
 1..59
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="ax42f06"
 /clone_1b="Proliferating Human Erythroid Cells (LCB:ax
 library)"
 /sex="unknown"
 /tissue_type="blood"
 /cell_type="Erythroid Cells"
 /cell_line="Primary Culture of Peripheral Blood
 Mononuclear Cells"
 /dev_stage="Progenitor; EPO responsive CD71++++"
 /lab_host="SOLR"
 /note="Organ: blood; Vector: Lambda ZAP II; Site 1: EcoRI;
 Site 2: EcoRI; 65,000 proliferating erythroid cells from
 the buffy coat of a blood donation were obtained by flow
 cytometric separation after a 5-day culture period in the
 presence of erythropoietin. Total RNA was purified from
 the sorted cell population using RNeasy reagent. RNA (0.3
 ug) was converted into double stranded cDNA using
 Clontech's Capfinder cDNA Library Construction Kit
 (Clontech) according to the manufacturer's protocol and
 cloned into EcoRI digested Lambda Zap II vector
 (Stratagene). The phage library was amplified once prior
 to in vivo excision in SOLR cells. Individual colonies
 were grown, and the cDNA inserts were sequenced in high
 throughput (NIH Intramural Sequencing Center
 http://www.nisc.nih.gov/)."

BASE COUNT
 0 a 7 c 1 g 51 t

ORIGIN

Query Match 0.9%; Score 22.2; DB 13; Length 59;
Best Local Similarity 69.8%; Pred. No. 1.8e+06;
Matches 30; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1760 AAAAAATCAATGTCGCAAAAAAAGCTTAAGCAAAATA 1802
 Db 50 AAAAAAAAAAAAAAAAAAGAAAAAAGAAAAAAGAAAAA 8

RESULT 42
LOCUS AA014672 49 bp mRNA linear EST 21-JAN-1997
DEFINITION mh30b01.r1 Soares mouse placenta 4bmkp13.5 14.5 Mus musculus cDNA
 clone IMAGE:443977 5', mRNA sequence.
ACCESSION AA014672
VERSION AA014672.1 GI:1475759
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 49)
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Maria,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Stepcoe,M., Tan,F., Underwood,K., Moore,B.,


```

/deb stage="20 week-post conception fetus"
/lab_host="rdh10B (ampicillin resistant)"
/notes="Organ: Liver and Spleen; Vector: pT7n3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
liver spleen INFs library. 1st strand cDNA was primed
with a Pac I - oligo(dT) primer [5',
AACGGAAGATTAATTAACATCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT7n3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo."

```

DEFINITION	r199d01.v1 Meloidogyne javanica egg PAMP1 v6 Chiapelli McCarter					
ACCESSION	B1745330					
VERSION	B1745330.1 GI:15767132					
KEYWORDS	EST.					
ORGANISM	root-knot nematode. Meloidogyne javanica Eukaryotes; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.					
REFERENCE	1 (bases 1 to 57) McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Rittler,E., Bennett,J., Franklin,C., Tsagarisvilli,R., Ronto,I., Kennedy,S., Magnute,L., Beck,C., Underwood,K., Steptoe, 'M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Korn,S., ,Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.					
TITLE	The Washington Univ. Nematode EST Project, 1999					
JOURNAL	Unpublished (1999)					
COMMENT	Contact: McCarter JP The Washington Univ. Nematode EST Project, 1999. Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu The library was constructed by Brandi Chiapelli and Dr. James McCarter (bbchiapel@watson.wustl.edu & jmcarter@watson.wustl.edu) at Washington University, St. Louis. DNA Sequencing by: Washington University Genome Sequencing Center St. Louis. Location/Qualifiers 1..57 /organism="Meloidogyne javanica" /db_xref="taxon:6303" /clone_lib="Meloidogyne javanica egg PAMP1 v6 Chiapelli McCarter" /dev_stage="enriched for eggs" /lab_host="DH10B" /note="Vector: PAMP1 (Gibco); The library was constructed by Brandi Chiapelli and Dr. James McCarter at Washington University, St. Louis. The cdna was made by using Dynabead oligo-dT priming (Dynal). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of PAMP1. Nematodes were provided by Dr. David Bird of North Carolina State University."					
BASE COUNT	26 a 1 c 4 g 26 t					
ORIGIN						
Query Match	0.9%; Score 22; DB 13; Length 57;					
Best Local Similarity	63.0%; Pred. No. 2e+06;					
Matches 34; Conservative	0; Mismatches 20; Indels 0; Gaps 0;					
Cy 1749	ACGGGAGTTTAAAAATCATCAATCGTCGCAAAAAAAAAACTTAAGCAAATA 1802					
Dn 56	ACTTTTTTTTTTTAAACAATCATTATTTAAAAAATAATATTAATCAATAA 3					
RESULT 47						
B1842365/c	58 bp mRNA linear EST 04-OCT-2001					
LOCUS						
DEFINITION	f482g06.y1 zebrafish neuronal Danio rerio cdna clone 486962 5', mRNA sequence.					
ACCESSION	B1842365					
VERSION	B1842365.1 GI:15954888					
KEYWORDS	EST.					
SOURCE	zebrafish.					
ORGANISM	Danio rerio Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes ; Cyprinidae; Danio. 1 (bases 1 to 58) Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy					

TITLE The Washington Univ. Nemacode EST Project, 1999
JOURNAL Unpublished (1999)
COMMENT Contact: McCarter JP
The Washington Univ. Nemacode EST Project, 1999
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. DNA Sequencing by: Washington

/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-026E08-01.3759"

BASE COUNT 23 a 10 c 10 g 15 t

ORIGIN

Query Match 0.9%; Score 22; DB 17; Length 58;
Best Local Similarity 63.0%; Pred. No. 2e+06;
Matches 34; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 903 ATTCACTGGGAGATGAGAAAGAAACAAATTCCTCAATGTAAGTACT 956
Db 4 ATTCATTCGTTAATATATGCAAAAAGAGTTGCAAACTGCAATGATGACT 57

/clone lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC106. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

RESULT 50
AL779773 60 bp mRNA linear EST 25-JUN-2002
LOCUS AL779773 XGC-neurula Silurana tropicalis cDNA clone TNeu078a06 5',
DEFINITION mRNA sequence.

ACCESSION AL779773
VERSION AL779773.1 GI:21565477
KEYWORDS EST.
SOURCE western clawed frog.
ORGANISM Silurana tropicalis
Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae; Xenopodinae; Silurana.

REFERENCE 1 (bases 1 to 60)
AUTHORS Taylor,R., Ashurst,J.L., Croning,M.D.R., Zorn,A.M. and Rogers,J.
TITLE Sanger Xenopus tropicalis EST project 2002
JOURNAL Unpublished (2001)
COMMENT Contact: Taylor R

Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE ID: TNeu078a06.p1cSP6
Sequencing primer: P1cSP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
location/Qualifiers

FEATURES
source 1..60
/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="TNeu078a06"
/clone_lib="XGC-neurula"
/dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
/note="vector: pCS107; Site 1: EcoRI, Site 2: NotI; cDNA was oligo dt primed from 5ug of poly A+ RNA from neurula. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."

BASE COUNT 41 a 8 c 7 g 4 t

ORIGIN

Query Match 0.9%; Score 22; DB 9; Length 60;
Best Local Similarity 67.4%; Pred. No. 2e+06;
Matches 31; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1760 AAAAAATCAATCGTGCAGAAAGAAACTTAAGCAATAGTA 1805
Db 14 AAAAAATGAAAAAGAGAAACAAAAAATA 59

RESULT 51

BU059311 38 bp mRNA linear EST 11-DEC-2001
LOCUS BU059311 NIBB Mochii normalized Xenopus tailbud library Xenopus
DEFINITION laevis cDNA clone XL062d07 5', mRNA sequence.

ACCESSION BU059311.1 GI:17490829
VERSION BU059311.1
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae; Xenopodinae; Xenopus.

REFERENCE 1 (bases 1 to 38)
AUTHORS Kityama,A., Teraoka,C., Mochii,M., Ueno,N., Shin-I,T. and Kohara
Y.
TITLE Expressed genes in X. laevis embryo
JOURNAL Unpublished (2001)
COMMENT Contact: Tadao Shin-I
Center For Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES
source 1..38
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL062d07"
/clone_lib="NIBB Mochii normalized Xenopus tailbud library"
/tissue_type="whole embryo"
/dev_stage="stage 25"
/note="vector: pBSR3; Site 1: NotI, Site 2: EcoRI; cDNAs were oligo-dt primed and directionally cloned. Staging according to Newkoo and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn, (Wellcome/CRC Institute)."

BASE COUNT 15 a 1 c 1 g 18 t 3 others

ORIGIN

Query Match 0.9%; Score 21.8; DB 13; Length 38;
Best Local Similarity 72.2%; Pred. No. 2.3e+06;
Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2108 TCTTTTATATATATATATATATATTTTCAATAGA 2143
Db 1 TTTTATATATATATATATATATTTTAAANAAA 36

RESULT 52
BU057533 46 bp mRNA linear EST 10-DEC-2001
LOCUS BU057533 NIBB Mochii normalized Xenopus tailbud library Xenopus
DEFINITION laevis cDNA clone XL104f09 5', mRNA sequence.

ACCESSION BU057533
VERSION BU057533.1 GI:17479603
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae; Xenopodinae; Xenopus.

REFERENCE 1 (bases 1 to 46)
AUTHORS Kityama,A., Teraoka,C., Mochii,M., Ueno,N., Shin-I,T. and Kohara
Y.
TITLE Expressed genes in X. laevis embryo
JOURNAL Unpublished (2001)
COMMENT Contact: Tadao Shin-I
Center For Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856

WashU-HNMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:681245
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. 49
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:1310949"
/clone_1lb="Stratagene mouse macrophage (#937306)"
/tissue_type="macrophage"
/dev_stage="MEH1-3 cell line"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: blood; Vector: pBluescript SK-; Site 1:
ECORI; Site 2: XhoI; Cloned unidirectionally. Primer:
0.150 dt. MEH1-3 cell line. Average insert size: 1.5 kb;
Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATTCGGCGACGAG
3' -3' adaptor sequence: 5' CTCGAGTTT TTT TTT TTT TTT 3' "

BASE COUNT 9 a 12 c 15 g 13 t
ORIGIN

Query Match 0.9%; Score 21.8; DB 9; Length 49;
Best Local Similarity 65.3%; Pred. No. 2.3e+06;
Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 1903 TTAAAGGTAGATGTTCTGTAATCTGAGTGTGATGTGACAGA 1951
Db 1 TGAGGTCGCGATGCTGCTGTGACACTTGTGATCTACTGATCCCA 49

RESULT 56
AA823664 52 bp mRNA linear EST 17-FEB-1998
LOCUS
DEFINITION
v769d09.81 Knowles Solter mouse 2 cell Mus musculus cDNA clone
IMAGE:1125905 5' similar to gb:U03161 SERUM RESPONSE FACTOR (HUMAN
); mRNA sequence.
ACCESSION
AA823664
VERSION
AA823664.1 GI:2893532

KEYWORDS
house mouse.
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 52)
Marras, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Giesel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

REFERENCE
AUTHORS
The WashU-HNMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HNMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:615241.

TITLE
JOURNAL
COMMENT
Location/Qualifiers
1. 52
/organism="Mus musculus"

/strain="C57BL/6J x DBA/2J F1"
/db_xref="taxon:10090"
/clone="IMAGE:1125905"
/clone_1lb="Knowles Solter mouse 2 cell"
/tissue_type="embryo"
/dev_stage="2-cell"
/lab_host="DH108"
/note="Organ: embryo; Vector: pBluescribe (modified);
Site 1: Mui; Site 2: SalI; Cloned unidirectionally from
mRNA prepared from 13,500 2-cell stage embryos. Primer:
SalI (dt): 5'-CGGTGACGCGTGGACGCTTTT TTT TTT TTT 3'.
were cloned into the Mui/SalI sites of a modified
pBluescribe vector using commercial linkers (NEB).
Average insert size: 1.2 kb."

BASE COUNT 26 a 3 c 6 g 17 t
ORIGIN

Query Match 0.9%; Score 21.8; DB 9; Length 52;
Best Local Similarity 92.0%; Pred. No. 2.3e+06;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2117 TATATAATATATATTTTCAATA 2141
Db 21 TCTATAATAATATATTTTAAATA 45

RESULT 57
BH792320 52 bp DNA linear GSS 02-APR-2002
LOCUS
DEFINITION
SALK_063406.23.95.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_063406.23.95.x, DNA
sequence.
ACCESSION
BH792320
VERSION
BH792320.1 GI:19888967
KEYWORDS
GSS.
SOURCE
thale cress.
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 52)
Alonso, J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, R., Gadriab
, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P.,
Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 X1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.

TITLE
JOURNAL
COMMENT
Location/Qualifiers
1. 52
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_063406.23.95.x"
/clone_1lb="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 15 a 18 c 10 g 9 t
ORIGIN

Query Match 0.9%; Score 21.8; DB 17; Length 52;
 Best Local Similarity 78.8%; Pred. No. 2.3e+06;
 Matches 26; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1321 ATCCGATCCTCGAAGTTATTTGGCGCCCA 1353
 DB 20 ACCCTAACTCCTCGAAGTAATGAGGCCCA 52

RESULT 58 AU258750

LOCUS AU258750 54 bp mRNA linear EST 25-APR-2002
 DEFINITION AU258750 3'-directed mouse cDNA library Mus musculus cDNA clone
 BDD0013612 3', mRNA sequence.

ACCESSION AU258750
 VERSION AU258750.1 GI:20324614
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE Kato, K. and Matoba, R.
 AUTHORS Generation of expressed sequence tags from mouse brain
 TITLE Unpublished (2002)
 JOURNAL Contact: Kikuya Kato
 COMMENT Graduate School of Biological Sciences
 Nara Institute of Science and Technology
 8916-5 Takayama, Ikoma, Nara 630-0101, Japan
 Tel: 81-743-72-5581
 Fax: 81-743-72-5589
 Email: kato@bs.aisit-nara.ac.jp,
 URL: http://love2.aisit-nara.ac.jp/BS/BD/index.html.

FEATURES source

1..54
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="BDD0013612"
 /clone_lib="3'-directed mouse cDNA library"
 /tissue_type="brain"
 /note="Vector: pGEM-T-easy"
 /note="Vector: 7 g 21 t
 BASE COUNT 18 a 7 c 7 g 21 t 1 others
 ORIGIN

Query Match 0.9%; Score 21.8; DB 9; Length 54;
 Best Local Similarity 70.7%; Pred. No. 2.2e+06;
 Matches 23; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2099 CAACCTGAATCTTTTATATATAATATATATTTTCAA 2139
 DB 14 GCACCTGATTTTGTGTTAATAATAAGTTTGATATAA 54

RESULT 59
 AI888083 55 bp mRNA linear EST 01-SEP-1999
 LOCUS AI888083/3
 DEFINITION W22907.x1 NCI_CGAP_Ur4 Homo sapiens cDNA clone IMAGE:2437404 3',
 mRNA sequence.

ACCESSION AI888083
 VERSION AI888083.1 GI:5593247
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-rc@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLAT at:
 www-bio.lim.gov/bdip/image/image.html
 Seq primer: -400P from Gibco.

FEATURES source

1..55
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2437404"
 /clone_lib="NCI_CGAP_Ur4"
 /tissue_type="serous papillary carcinoma, high grade, 2
 pooled tumors"
 /lab_host="DH10B"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.48 kb. Life Technologies catalog #:
 11542-016"

BASE COUNT 20 a 2 c 9 g 24 t

Query Match 0.9%; Score 21.8; DB 9; Length 55;
 Best Local Similarity 70.7%; Pred. No. 2.2e+06;
 Matches 23; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2101 ACCGATCCTTTTATATATAATATATATTTTCAA 2141
 DB 45 ACCGATGCTCTACTACCAATTAATATATTTAAATA 5

RESULT 60
 AZ331030 55 bp DNA linear GSS 29-SEP-2000
 LOCUS AZ331030
 DEFINITION IN0056G09R Mouse 10kb plasmid UGCLIM library Mus musculus genomic
 clone UGCLIM0056G09 R, DNA sequence.

ACCESSION AZ331030
 VERSION AZ331030.1 GI:10393153
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 55)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Relly,
 M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
 Plate: 0056 row: G column: 09
 Seq primer: CACACAGAAACGATGACC
 Class: plasmid ends
 High quality sequence stop: 55.

FEATURES source

1..55
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCLIM0056G09"
 /clone_lib="Mouse 10kb plasmid UGCLIM library"

/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD29uv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD29 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid p1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 29 a 7 c 7 g 12 t

Query Match 0.9%; Score 21.8; DB 17; Length 55;
Best Local Similarity 70.7%; Pred. No. 2.2e+06;
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1798 AATAGTGTCTGACTTACGACATCAATTAATGAT 1838
Db 2 AATATAATATGTAAGAAACCTTACCAATCAATTAAGAT 42

RESULT 61 58 bp mRNA linear EST 12-JAN-2001
LOCUS BF791590 602251706F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4344312 5',
mRNA sequence.
ACCESSION BF791590
VERSION BF791590.1 GI:12096644
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 58)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LHAM962 row: k column: 01
High quality sequence stop: 58.

FEATURES
source location/Qualifiers

1..58
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4344312"
/clone_id="NIH_MGC_84"
/tissue_type="adrenal cortex carcinoma, cell line"
/lab host="DH10B (phage-resistant)"
/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dr primed. Average insert size 1.229 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

BASE COUNT 49 a 1 c 2 g 6 t

Query Match 0.9%; Score 21.8; DB 12; Length 58;
Best Local Similarity 65.3%; Pred. No. 2.2e+06;
Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 1755 ATTAAAAATCAATGATGCAAAAAAATTAAGCAAAATG 1803
Db 10 ATGTTAAAAAATCAATGATGCAAAAAAATTAAGCAAAATG 58

RESULT 62 58 bp mRNA linear EST 04-OCT-2001
LOCUS B1846606/c f880906.x1 Zebrafish neuronal Danio rerio cDNA clone 4886602 3',
mRNA sequence.
ACCESSION B1846606
VERSION B1846606.1 GI:15959129
KEYWORDS EST.
SOURCE zebrafish.
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 58)
AUTHORS Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
TITLE Mashu Zebrafish EST Project 1998
JOURNAL Unpublished (1998)
COMMENT Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrfish@watson.wustl.edu
CDNA Library constructed by S. Lin DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: the I.M.A.G.E. Consortium/LNL, send email to: info@image.llnl.gov
Seq primer: T7 from Gibco.

FEATURES
source location/Qualifiers

1..58
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone="4886602"
/clone_id="Zebrafish neuronal"
/sex="mixed"
/dev_stage="adult"
/lab host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: pBluescript (modified); Site 1: DraIII(Y); Site 2: DraIII(X); Library is cloned directionally between the DraIII(X) and DraIII(Y) sites and has been amplified. Library constructed by S. Lin."

BASE COUNT 8 a 4 c 2 g 44 t

Query Match 0.9%; Score 21.8; DB 13; Length 58;
Best Local Similarity 61.4%; Pred. No. 2.2e+06;
Matches 35; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 1744 AATTAAGTGTGATTTTAAATATCAATGATGCAAAAAAATTAAGCAAAA 1800
Db 57 AATTAATTAATGTTAAAGCAATTAATATGAAAAAATTAAGCAAAA 1

RESULT 63 59 bp mRNA linear EST 02-JAN-1998
LOCUS AA726911/v37b05.r1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone
DEFINITION

IMAGE:1193553 5', mRNA sequence.

AA726911.1 GI:2744618

EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 59)
Matta,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,,
Geisel,S., Kucabada,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Thelsing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMNI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMNI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel.: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MG1:640643
Seq primer: -28ml3 rev1 ET from Amersham.

FEATURES
source
1..59
Location/Qualifiers
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:1193553"
/clone_lib="Stratagene mouse Tcell 937311"
/tissue_type="Tcell"
/dev_stage="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: blood; Vector: plasmid construct SK-; Site: 1:
EcoRI; Site: 2: XhoI; Cloned unidirectionally. Primer:
O150 dt. M30 CD4+ cells. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGCGACGAC
3' -3' adaptor sequence: 5' CTCGAGTCTTTTCTTTT 3'."

BASE COUNT
31 a 4 c 4 g 20 t

ORIGIN
Query Match 0.9%; Score 21.8; DB 9; Length 59;
Best Local Similarity 61.4%; Pred. No. 2.2e+06;
Matches 35; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
Oy 2112 TTTTATATATATATATATTTTCAAAATAGATTTTGCATTCAGCTCATATGAAA 2168
Db 59 TTTTATATATATATATATTTTAAAGAAAAATTCATATTTATTTCAAGACATCATGAAA 3

RESULT 64
LOCUS
AA547914
DEFINITION
M83D6V2G01T3 Brugia malayi day 6 post-infection third stage larvae
SAB96MTM-Bml3d6 Brugia malayi cDNA clone 3d6V2G01 5', mRNA
sequence.
ACCESSION
AA547914
VERSION
AA547914.1 GI:2315115
KEYWORDS
EST.
SOURCE
Brugia malayi.
ORGANISM
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidae;
Onchocercidae; Brugia.
1 (bases 1 to 60)
Blaxter,M.L., Waterfall,M., Daub,J., Licotte-Waniewski,M., Baron,L.
and Jones,S.J.
Genes expressed in day six post-infection, third stage larvae of
Brugia malayi
Unpublished (1997)
Contact: Blaxter ML

JOURNAL
COMMENT

Institute of Cell, Animal and Population Biology
 University of Edinburgh
 Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
 3JT, UK.
 Tel: +44 131 650 6760
 Fax: +44 131 670 5450
 Email: mark.blaxter@ed.ac.uk
 The ABI trace of this sequence can be viewed at
<http://www.sanger.ac.uk/brugia/3D6/MB3D6V2G01T3.html>
 Seq primer: T3.

FEATURES
 source
 Location/Qualifiers
 1..60
 /organism="Brugia malayi"
 /strain="R3 Labs"
 /db_xref="taxon:6279"
 /clone="3D6V2G01"
 /clone_1lb="Brugia malayi day 6 post-infection third stages
 larvae SAW96MLW-Bml3d6"
 /sex="mixed"
 /dev_stage="third stage larvae, six days after infection"
 /lab_host="E. coli XL1-Blue"
 /note="Vector: lambdaZapIT (Unizap XN); Site_1: Eco R I
 (5' end); Site_2: Xho I (3' end); Brugia malayi is a
 lymphatic filarial nematode parasite of humans. mRNA was
 prepared from third stage larvae of Brugia malayi isolated
 from the peritoneal cavity of jirds six days after
 infection. The mRNA was converted to double stranded cDNA
 using reverse transcriptase and oligo(dT) followed by
 Rnase H and DNapol I. The library had 2 x 10E5 independent
 recombinants and average insert size was 900 base pairs.
 The library was constructed by Michelle Lizotte-Waniewski.
 The library is available from The Filarial Gene Project
 Resource Center: contact Dr. S.A. Williams, Clark Science
 Center, Smith College, Northampton, MA 01063 USA phone +1
 413 585 3826 fax +1 413 585 3786 email genomes@smith.edu."

BASE COUNT
 14 a 0 c 2 g 44 t

ORIGIN
 Query Match 0.9%; Score 21.8; DB 9; Length 60;
 Best Local Similarity 70.7%; Pred.No. 2.2e+06;
 Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Oy 2111 TTTTATTAATAATATATATTTTTCAAATGATTTTGTAT 2151
 Db 12 TGTATTAAATAATATATATTTTTCATGTTTAT 52

RESULT 65
 LOCUS BB896253 45 bp linear EST 20-OCT-2000
 DEFINITION 601438976.F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3923778 5',
 mRNA sequence.
 ACCESSION BB896253
 VERSION BB896253.1 GI:10360469
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 45)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs@emall.nih.gov
 Tissue Procurement: ATCC/DCTP/DRP
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLML)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLML at:
<http://image.llnl.gov>
 Plate: LLM9760 row: h column: 19

Plate: 44 row: e column: 07
Seq primer: M13R1 reverse primer (AB1).
Location/Qualifiers

FEATURES

SOURCE

1. .54
/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="g144e07"
/clone_1lb="Mouse Organ of Corti cDNA pluescript"
/sex="male and female"
/stage="Post natal day 5 to 13"
/note="Organ: Organ of Corti; Vector: pluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exassist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGTATGACC) and 25x strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT

16 a 9 c 26 g 3 t

Query Match 0.9%; Score 21.6; DB 14; Length 54;
Best Local Similarity 63.5%; Pred. No. 2.5e+06;
Matches 33; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 117 AGACCTGACCGACGAGAGCGGCTCTGAGATGACTGGAGGAGCG 168
DB 3 AGACGGGAGGACCACTGACCAAGGCTCTGACGAGAGGAGAGGAGG 54

RESULT 69
BH846951
LOCUS
DEFINITION
54 bp DNA linear GSS 13-JUN-2002
SALK_012126.50.20.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_012126.50.20.x, DNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
GSS.
BH846951.1 GI:21417822
thale cress.

Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 54)
Alonso, J.M., Lelise, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J., and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.
Location/Qualifiers

FEATURES

SOURCE

1. .54
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_012126.50.20.x"
/clone_1lb="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence, at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT 19 a 2 c 5 g 28 t
ORIGIN

Query Match 0.9%; Score 21.6; DB 17; Length 54;
Best Local Similarity 68.2%; Pred. No. 2.5e+06;
Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
OY 2111 TTTTATATATATATATATATTTTCAATAGATTGTGATCA 2154
DB 7 TTTTATATATATATATATATTTTCTAAATTAATGTTATATTTA 50

RESULT 70

LOCUS

AL786691

DEFINITION

AL786691 XGC-neurula silurana tropicalis cDNA clone TNeu09em20 5', mRNA sequence.

ACCESSION

AL786691

VERSION

AL786691.1 GI:21572395

KEYWORDS

EST.

SOURCE

ORGANISM

Western clawed frog.

Silurana tropicalis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

ORGANISM
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.

REFERENCE
1 (bases 1 to 58)

AUTHORS
Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurk,R., Ritter,E.,
Kohn,S., Shih,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
and Wilson,R.

TITLE
Washu Zebrafish EST Project 1998

JOURNAL
Unpublished (1998)

COMMENT
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbratish@wustl.edu
cDNA library construction by: Joe Barnes and Steve Johnson. DNA
Sequencing by: Washington University Genome Sequencing Center Clone
distribution: Research Genetics web address:
<http://www.researchgenetics.com/>
Putative full length read
The vector to vector length is 59
Seq primer: T3 ET from Amersham.

FEATURES
source
1..58
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone="4962547"
/clone_lib="Zebrafish SJD day 8 fin regeneration"
/sex="male"
/issue_type="fin, 8-day regeneration"
/lab_host="DH10B"
/note="Vector: pAMP1, Site 1: EcoRI, Site 2: NotI. First
strand cDNA synthesis was primed using oligo-dT on
magnetic beads with an additional primer
5'-ggcgccgtatcagctacta-tagg-3'. Second strand
synthesis was a 3-cycle PCR using the primers
5'-ggcgccgtatcagctacta-tagg-3' and
5'-aagcagtggtacacagcagagctt-tttttttttt-3'. cDNA
was subsequently amplified in a 7-cycle PCR with the
following primers: 5'-ggcgccgtatcagctacta-tagg-3' and
5'-aagcagtggt-acacacgcag. Deoxy-UMP adaptors were added in
a third PCR (5 cycles) and the primers
5'-caucaucaucaugccgtatcagctacta-tagg-3' and
5'-cucacucaucaagcagctacta-tagg-3'. Ends were
treated with uracil DNA glycosylase and product with 3'
overhangs was annealed to complementary ends of pAMP1.
Insert can be excised using EcoRI and NotI. Library
constructed by Joe Barnes and Steve Johnson (Washington
University)."

BASE COUNT
41 a 0 c 5 g 12 t

ORIGIN
Query Match 0.9%; Score 21.6; DB 13; Length 58;
Best Local Similarity 63.5%; Pred. No. 2.5e+06;
Matches 33; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 2110 TTTTATTAATAATATTTTCAATGATTTTGAATTCAGCTCATT 2161
|||||
Db 58 TTTTATTTTATTTTATTAATAATTTTATTTATTTTCCATT 7

RESULT 74
BI709260 58 bp mRNA linear EST 19-SEP-2001
LOCUS B622b03.Y1 Zebrafish SJD day 8 fin regeneration Danio rerio cDNA
DEFINITION clone 50722212 5', mRNA sequence.
ACCESSION BI709260
VERSION BI709260.1 GI:15684955
KEYWORDS EST.
SOURCE zebrafish.

ORGANISM
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.

REFERENCE
1 (bases 1 to 58)

AUTHORS
Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurk,R., Ritter,E.,
Kohn,S., Shih,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
and Wilson,R.

TITLE
Washu Zebrafish EST Project 1998

JOURNAL
Unpublished (1998)

COMMENT
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbratish@wustl.edu
cDNA library construction by: Joe Barnes and Steve Johnson. DNA
Sequencing by: Washington University Genome Sequencing Center Clone
distribution: Research Genetics web address:
<http://www.researchgenetics.com/>
Putative full length read
The vector to vector length is 59
Seq primer: T3 ET from Amersham.

FEATURES
source
1..58
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone="5072212"
/clone_lib="Zebrafish SJD day 8 fin regeneration"
/sex="male"
/issue_type="fin, 8-day regeneration"
/lab_host="DH10B"
/note="Vector: pAMP1, Site 1: EcoRI, Site 2: NotI. First
strand cDNA synthesis was primed using oligo-dT on
magnetic beads with an additional primer
5'-ggcgccgtatcagctacta-tagg-3'. Second strand
synthesis was a 3-cycle PCR using the primers
5'-ggcgccgtatcagctacta-tagg-3' and
5'-aagcagtggtacacagcagagctt-tttttttttt-3'. cDNA
was subsequently amplified in a 7-cycle PCR with the
following primers: 5'-ggcgccgtatcagctacta-tagg-3' and
5'-aagcagtggt-acacacgcag. Deoxy-UMP adaptors were added in
a third PCR (5 cycles) and the primers
5'-caucaucaucaugccgtatcagctacta-tagg-3' and
5'-cucacucaucaagcagctacta-tagg-3'. Ends were
treated with uracil DNA glycosylase and product with 3'
overhangs was annealed to complementary ends of pAMP1.
Insert can be excised using EcoRI and NotI. Library
constructed by Joe Barnes and Steve Johnson (Washington
University)."

BASE COUNT
41 a 0 c 5 g 12 t

ORIGIN
Query Match 0.9%; Score 21.6; DB 13; Length 58;
Best Local Similarity 63.5%; Pred. No. 2.5e+06;
Matches 33; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 2110 TTTTATTAATAATATTTTCAATGATTTTGAATTCAGCTCATT 2161
|||||
Db 58 TTTTATTTTATTTTATTAATAATTTTATTTATTTTCCATT 7

RESULT 75
BI496827 59 bp mRNA linear EST 28-AUG-2001
LOCUS B1496827
DEFINITION dE128f02.w1 Morton Fetal Cochlea Homo sapiens cDNA clone
IMAGE:2538387 3', mRNA sequence.
ACCESSION BI496827
VERSION BI496827.1 GI:15336171
KEYWORDS EST.

SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 59) Robertson,N.G., Khearpal,U., Gutierrez-Espeleta,G.A., Bieber,F.R. and Morton,C.C.
TITLE	Isolation of novel and known genes from a human fetal cochlear cDNA library using subtractive hybridization and differential screening
JOURNAL	Genomics 23, 42-50 (1994)
MEDLINE	95130111
COMMENT	Contact: Morton, C. C. Departments of Pathology and Obstetrics, Gynecology and Reproductive Biology Brigham and Women's Hospital 75 Francis Street, Harvard Medical School, Boston, MA 02115, USA Tel: 617 732 7980 Fax: 617 738 6996 Email: ccmorton@rics.bwh.harvard.edu DNA sequencing and analyses were performed by National Institutes of Health Intramural Sequencing Center (NISC; see http://www.nisc.nih.gov). This clone is available royalty-free through LIND; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Plate: L14M6322 row: L column: 4 Seq primer: T7 primer. Location/Qualifiers 1..59 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:2538387" /clone_lib="Morton Fetal Cochlea" /tissue_type="cochlea" /dev_stage="16-22 week fetus" /lab_host="SOLR cells (kanamycin resistant)" /note="organ: ear; Vector: Bluescript SK-; Site 1: EcoRI Site 2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned unidirectionally. Primer: 0.150 dt. Fetal cochlea, normal 37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP XR Vector. Library constructed by N. Robertson, C. Morton. -5' adaptor sequence: 5' GAATTCGGACGACGG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' "
BASE COUNT	9 a 11 c 8 g 31 t
ORIGIN	
Query Match	0.9%; Score 21.6; DB 13; Length 59;
Best Local Similarity	85.7%; Pred. No.2.5e+06;
Matches 24; Conservative	0; Mismatches 4; Indels 0; Gaps 0;
QY 2108	TCCTTTTATATATAATATATATATTTT 2135
Db 24	TTTTTTTATATATATATGATTTTAT 51
RESULT 76	
BG348123/c	60 bp mRNA linear EST 28-FEB-2001
LOCUS	de78905.Y1 Kirschner embryo St10 14 Xenopus laevis cDNA clone
DEFINITION	IMAGE:3518001 5', mRNA sequence.
ACCESSION	BG348123
VERSION	BG348123.1 GI:13168549
KEYWORDS	EST.
SOURCE	African clawed frog.
ORGANISM	Xenopus laevis
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus.
AUTHORS	1 (bases 1 to 60) Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Miller,L., Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R., Waterston,R. and Wilson,R.
TITLE	Maenh Xenopus EST project, 1999

JOURNAL COMMENT

Unpublished (1999)
Contact: Sandy Clifton, Ph. D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library constructed by M. Kirschner (Harvard Medical School). DNA
Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/HLNLT at: info@image.llnl.gov
Seq primer: -40BP from GIBCO.

FEATURES

Source

1..60
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:3518001"
/clone_lib="Kirschner embryo St10 14"
/tissue_type="pooled embryos (stage 10-14)"
/lab_host="DH10B (phage-resistant)"
/note="Vector: PCS2+; Site 1: NotI; Site 2: SalI;
Size selected for average insert size 1.2 kb. Library was
constructed and donated by M. Kirschner (Harvard Medical
School)."

BASE COUNT 32 a 3 c 5 g 20 t

ORIGIN

Query Match 0.9%; Score 21.6; DB 12; Length 60;
Best Local Similarity 60.0%; Pred. No. 2.5e+06;
Matches 36; Conservative 0; Mismatches 24; Indels 0; Gaps 0

Qy 2109 CTTTCTTTTATATATAATATATTTTCAATAGATTTTGATTGAGCTCATATGAAA 2168
|||||
Db 60 CTTTCTTTTATATATATATATTTTCAATAGATTTTGATTGAGCTCATATGAAA 1
|||||

RESULT 77

LOCUS C25778 60 bp mRNA linear EST 29-JUL-1997
DEFINITION C25778 Dictyostelium discoideum FC (H.Urushihara) Dictyostelium
discoideum cDNA clone FC-BC03, mRNA sequence.

ACCESSION C25778
VERSION C25778.1 GI:2282564
KEYWORDS EST.
ORGANISM Dictyostelium discoideum.
SOURCE Dictyostelium discoideum
Eukaryota; Eukaryota; Dictyostelid; Dictyostelium.
REFERENCE 1 (bases 1 to 60)
AUTHORS Suzuki,K., Shimizu,H. and Urushihara,H.
TITLE Sexual cDNA in D. discoideum(970724)
JOURNAL Unpublished (1997)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.
Location/Qualifiers

FEATURES

Source

1...60
/organism="Dictyostelium discoideum"
/strain="XAX3"
/db_xref="taxon:44689"
/clone_lib="PC-BC03"
/clone_lib="Dictyostelium discoideum FC (H.Urushihara)"

BASE COUNT 46 a 1 c 2 g 11 t

ORIGIN

Query Match 0.9%; Score 21.6; DB 14; Length 60;
Best Local Similarity 68.2%; Pred. No. 2.5e+06;
Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0

Oy	2108	TCTTTTATATAAATATATATTTTCACAAATGATTTCAT	2151
Db	50	TATTTTTTTTTTTTAATATATTTTTTTTTTATCAAGTTAT	7
RESULT 78			
LOCUS	N81844/c		
DEFINITION	TG9STxy4g903.r1 TgrH Tachyzoite cDNA Toxoplasma gondii clone	60 bp	mRNA linear EST 22-MAY-2000
ACCESSION	N81844		
VERSION	N81844.1	GI:1257597	
KEYWORDS	EST.		
SOURCE	Toxoplasma gondii.		
ORGANISM	Toxoplasma gondii.		
REFERENCE	Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;		
AUTHORS	Sarcocystidae; Toxoplasma.		
	1 (bases 1 to 60)		
	Hehl, A., Manger, I., Marra, M., Sibley, L.D., Ajioke, J.A., Aslett, M.A.,		
	'Dierrich, N.', Dubnueque, T., Hillier, L., Kucaba, T., Wan, K.L.,		
	Waterston, R.H. and Boothroyd, J.		
	WashU-Merck-Stanford-NIH Toxoplasma EST project		
	Unpublished (1996)		
	Contact: Marra M		
	Washington University School of Medicine		
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108		
	Tel: 314 286 1800		
	Fax: 314 286 1810		
	Email: toxo@watson.wustl.edu		
	David Sibley at toxest@borcim.wustl.edu for further information		
	relating to organism, clone or library availability.		
	Seq primer: T3		
	High quality sequence stop: 50.		
FEATURES			
source	Location/Qualifiers		
	1..60		
	/organism="Toxoplasma gondii"		
	/strain="RH"		
	/db_xref="caxon:5811"		
	/clone="tgzy4g903.r1"		
	/clone_lib="TgrH Tachyzoite cDNA"		
	/lab_host="YLI-Blue MRP."		
	/note="vector: Lambda ZAP; Site 1: EcoRI; Site 2: XhoI;		
	Toxoplasma RH strain tachyzoites were grown in human		
	foreskin fibroblast cultures in vitro. The library was		
	synthesized from polyA RNAs by oligo d(T) priming and		
	directionally cloned into the EcoI to XhoI sites of the		
	Lambda Zapri vector using the ZAP-cDNA synthesis kit		
	(Stratagene). WARNING: the library contains a small		
	percentage of cDNAs derived from the human host cells."		
	percentage of cDNAs derived from the human host cells."		
BASE COUNT	10 a 0 c 11 g 39 t		
ORIGIN			
Query Match	0.9%; Score 21.6; DB 14; Length 60;		
Best Local Similarity	60.0%; Pred. No. 2.5e+06;		
Matches	36; Conservative 0; Mismatches 24; Indels 0; Gaps 0;		
Oy	916	AATAGGAAGAACAATGCACAAATCCCAATGTGAACCAATTGGCCTCCCTACCTC	975
Db	60	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACTCTCTCTCTCTCTCTC	1
RESULT 79			
LOCUS	AZ368409/c	41 bp	DNA linear GSS 02-OCT-2000
DEFINITION	IM01B18x04R Mouse 10kb plasmid UUCGM library Mus musculus genomic		
ACCESSION	AZ368409		
VERSION	AZ368409.1	GI:10482109	
KEYWORDS	GSS.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		

REFERENCE
AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murineae; Mus-
1 (bases 1 to 41)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Petersen,T., Kelly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., STC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0118 row: A column: 04
Seq primer: CACGAGGAACACTTATGACC
Class: plasmid ends
High quality sequence stop: 41.
Location/Qualifiers
1. .41
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGM0118A04"
/clone_lib="Mouse 10kb plasmid UUCGM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from The Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (GI|4732114|GB|AF29072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES
SOURCE

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 71.8%; Pred. No. 2.8e+06;
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Oy 2108 TCTTTTATTATAATATATATATTTCAATGATTT 2146
|||||||
Db 40 TTTTTTTTCTTTAAAGATTATTTATTTAGTAATCT 2
|||||||

RESULT 80
LOCUS AI431480 46 bp mRNA linear EST 09-MAR-1999
DEFINITION th0f03.x1 NCI CGAP Lym12 Homo sapiens clone IMAGE:2120765 3'
similar to TR:Q26195 Q26195 FVAL GENE.; mRNA sequence.
ACCESSION AI431480 GI:4303480
VERSION AI431480.1
KEYWORDS EST.
SOURCE human
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 46)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www.bio.lim.gov/bdrp/image/image.html

BASE COUNT Trace considered overall poor quality
ORIGIN Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. .46
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="2120765"
/clone_lib="NCI-CGAP_Lym12"
/issue_type="Lymphoma, follicular mixed small and large
cell"
/lab_host="DH10B"
/note="Organ: lymph node; Vector: pCMV-SPORT6; Site: 1;
Salt: Site 2: NotI; Cloned unidirectionally. Primer:
Oligo dt. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015" 3 t

BASE COUNT 26 a 1 c 16 g 3 t

Query Match 0.9%; Score 21.4; DB 9; Length 46;
Best Local Similarity 80.6%; Pred. No. 2.8e+06;
Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Db 2041 AGGCAAAATGGGAAGCAAGCAAAAGAA 2071
2 AGGCATTAAGGGAAGGTAAAGAAATATATAA 32

RESULT 81
LOCUS BG222966 49 bp mRNA linear EST 07-FEB-2001
DEFINITION nah40b02.x1 NCI-CGAP_HN21 Homo sapiens cDNA IMAGE:4233530 3',
mRNA sequence.
ACCESSION BG222966
VERSION BG222966.1 GI:12708487
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 49)
NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Dental Research,
Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
CDNA Library Preparation: David B. Kitzman, Ph.D.
DNA Sequencing by: The I.M.A.G.E. Consortium (LINL)
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL, send email to:
infoimage.lim.gov
Seq primer: -40UP from Gibco.
Location/Qualifiers
1. .49
/organism="Homo sapiens"
/db_xref="taxon:9606"

FEATURES
source

/clone_image="4233530"
/clone_lib="NCI-CGAP_HN21"
/issue_type="nasopharyngeal carcinoma"
/lab_host="DH10B"
/note="Organ: head/neck; Vector: pAMP1; mRNA made from
head/neck tumor; cDNA made by oligo-dt priming.
directionally cloned into UDG sites. Size-selected on
agarose gel, average insert size 300 bp. Primary library.
cDNA library preparation: David B. Kitzman, Ph.D."

BASE COUNT 11 a 11 c 9 g 18 t
ORIGIN
Query Match 0.9%; Score 21.4; DB 12; Length 49;
Best Local Similarity 66.0%; Pred. No. 2.8e+06;
Matches 31; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
Db 203 TTGACCATATGAACTTGGCATGGAACATTGTGAATTTGAATC 249
1 TTTTCTTATGAGCATGTCCTCATCATGTGAGAGCTTGAATTC 47

RESULT 82
LOCUS BJ064587 51 bp mRNA linear EST 10-DEC-2001
DEFINITION BJ064587 NIBB Mochii normalized Xenopus tailbud library Xenopus
laevis cDNA clone XL080b20 5', mRNA sequence.
ACCESSION BJ064587
VERSION BJ064587.1 GI:17471537
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 51)
Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara
Y.

REFERENCE 1
AUTHORS Y.
TITLE Expressed genes in X. laevis embryo
JOURNAL Unpublished (2001)
COMMENT Contact: Tadao Shin-i
Center For Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tehni@genes.nig.ac.jp.
Location/Qualifiers
1. .51
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone_image="XL080b20"
/clone_lib="NIBB Mochii normalized Xenopus tailbud
library"
/issue_type="whole embryo"
/dev stage="stage 25"
/note="Vector: pBSRN3; Site 1: NotI; Site 2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library is subtracted
and was constructed by N. Garrett and A.M. Zorn,
(Wellcome/CRC Institute)."

FEATURES
source

BASE COUNT 27 a 0 c 5 g 19 t

Query Match 0.9%; Score 21.4; DB 13; Length 51;
Best Local Similarity 71.8%; Pred. No. 2.8e+06;
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Db 2108 TCTTTTATATATATATATATATTTTCAATAGATT 2146
48 TTTTCTTCAAAATTAATTTATTTTAAATATATAT 10

RESULT 83

BG271387 52 bp mRNA linear EST 20-FEB-2001
 LOCUS na149b05.x1 NCI_CGAP_HN20 Homo sapiens cDNA clone IMAGE:4263776 3',
 DEFINITION mRNA sequence.
 ACCESSION BG271387 GI:12979476
 VERSION BG271387.1
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 52)
 NCBI/NIH-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute / National Institute of Dental Research,
 Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 Unpublished (1997)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgaps-remail.nih.gov
 CNA Library Preparation: David B. Krizman, Ph.D.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL, send email to:
 info@image.llnl.gov
 Seq primer: -40UP from Gibco.
 Location/Qualifiers
 1..52
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_id="NCI_CGAP_HN20"
 /lab_host="DH10B"
 /note="Organ: normal head/neck tissue; Vector: PAMPL; mRNA
 made from head/neck tissue. cDNA made by oligo-dt
 priming. Directionally cloned into UDG sites.
 Size-selected on agarose gel, average insert size 300 bp.
 Primary library. cDNA Library Preparation: David B.
 Krizman, Ph.D."

BASE COUNT 12 a 12 c 10 g 18 t
 ORIGIN
 Query Match 0.9%; Score 21.4; DB 12; Length 52;
 Best Local Similarity 66.0%; Pred. No. 2.8e+06;
 Matches 31; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 203 TTGACCATATGAACTTGGCATGGAACATTGGAGAATTGAATC 249
 Db 1 TTTTCTTATGACATGTCCCGTACATCGTTAGAACCTTGAATTC 47

RESULT 84 53 bp mRNA linear EST 09-FEB-2001
 LOCUS na143b05.x1 NCI_CGAP_HN20 Homo sapiens cDNA clone IMAGE:4262744 3',
 DEFINITION mRNA sequence.
 ACCESSION BG231005
 VERSION BG231005.1 GI:12726083
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 53)
 NCBI/NIH-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute / National Institute of Dental Research,
 Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 Unpublished (1997)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgaps-remail.nih.gov
 CNA Library Preparation: David B. Krizman, Ph.D.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL, send email to:
 info@image.llnl.gov
 Seq primer: -40UP from Gibco.
 Location/Qualifiers
 1..53
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_id="IMAGE:4262744"
 /clone_lib="NCI_CGAP_HN20"
 /lab_host="DH10B"
 /note="Organ: normal head/neck tissue; Vector: PAMPL; mRNA
 made from head/neck tissue. cDNA made by oligo-dt
 priming. Directionally cloned into UDG sites.
 Size-selected on agarose gel, average insert size 300 bp.
 Primary library. cDNA Library Preparation: David B.
 Krizman, Ph.D."

BASE COUNT 10 a 11 c 8 g 24 t
 ORIGIN
 Query Match 0.9%; Score 21.4; DB 12; Length 53;
 Best Local Similarity 66.0%; Pred. No. 2.8e+06;
 Matches 31; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 203 TTGACCATATGAACTTGGCATGGAACATTGGAGAATTGAATC 249
 Db 7 TTTTCTTATGACATGTCCCGTACATCGTTAGAACCTTGAATTC 53

RESULT 85 55 bp DNA linear GSS 02-OCT-2000
 LOCUS A2366215
 DEFINITION IM0115A14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0115A14 F, DNA sequence.
 ACCESSION A2366215
 VERSION A2366215.1 GI:10479915
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 55)
 Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0115 row: A column: 14
 Seq primer: CGTTGTAAACGACGCCACT
 Class: plasmid ends
 High quality sequence stop: 55.
 Location/Qualifiers
 1..55
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_id="UUGC1M0115A14"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /note="Vector: PWD424V/ Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource

RESULT 88
AL7473426/c 59 bp mRNA linear EST 13-Apr-1999
LOCUS t13g01.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141424 3',
DEFINITION mRNA sequence.
ACCESSION AL7473426
VERSION AL7473426.1 GI:4326471
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 59)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/IML at:
www.bio.lim.gov/bdip/image/image.html
Insert Length: 1400 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 58.
Location/Qualifiers
1..59
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2141424"
/clone_id="NCI_CGAP_Gas4"
/tissue_type="poorly differentiated adenocarcinoma with
signed Tng cell features"
/lab_host="DH10B"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site: 1: Salt;
Site 2: Nct1; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"

BASE COUNT 8 a 0 c 2 g 49 t

ORIGIN

Query Match 0.9%; Score 21.4; DB 9; Length 59;
Best Local Similarity 66.0%; Pred. No. 2.8e+06;
Matches 31; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1756 TTTTAAATCATCATGTCGCAAAAATACTTAAGCAATA 1802
|||||
Db 53 TTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 89
AL769947/c 59 bp DNA linear GSS 19-JUN-2002
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-095A02-012025,
DEFINITION genomic survey sequence.
ACCESSION AL769947
VERSION AL769947.1 GI:21532149
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1
AUTHORS Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.
and Weisshaar, B.
TITLE A pipeline for automated high-throughput generation of ESTs

(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
Unpublished

REFERENCE
AUTHORS Rosso, M., Strizhov, N., Li, Y., Reis, B., Dekker, K. and Weisshaar, B.
TITLE A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
for flanking sequence tag based reverse genetics

JOURNAL Unpublished
REFERENCE 3 (bases 1 to 59)
AUTHORS Rosso, M., Li, Y., Strizhov, N. and Weisshaar, B.
TITLE Direct Substitution
JOURNAL Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
Zoectungsforchung, Carl-von-Linne-Weg 10, Koeln, 50629, Germany
COMMENT This sequence is recovered from the left border of the T-DNA. It
indicates an insertion close to or within gene At2g3880. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/
Location/Qualifiers
1..59
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-095A02-012025"
/clone_id="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC16. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thaliana nuclear genome sequence were
processed for submission. T-DNA derived sequences were
removed"

BASE COUNT 10 a 8 c 7 g 34 t

ORIGIN

Query Match 0.9%; Score 21.4; DB 17; Length 59;
Best Local Similarity 71.8%; Pred. No. 2.8e+06;
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2044 CMAATGGAGAGCAAGCAAGAACTTACCAATTG 2082
|||||
Db 57 CAATTGGGAATCCAAAAAATAAAAAAAAAAACAATTG 19

RESULT 90
AV837933 39 bp mRNA linear EST 07-NOV-2001
LOCUS AV837933/c
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-095A02-012025,
ACCESSION AV837933
VERSION AV837933.1 GI:16782084
KEYWORDS EST.
SOURCE Clona intestinalis.
ORGANISM Clona intestinalis.
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Clona.
REFERENCE 1 (bases 1 to 39)
AUTHORS Satoh, N., Satou, Y., Kohara, Y. and Shin-I, T.
TITLE Expressed genes in Clona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@acidian.zool.kyoto-u.ac.jp

FEATURES
source 1..39
Location/Qualifiers

```

/organism="Ciona intestinalis"
/db_xref="taxon:7719"
/clone="rcic101m15"
/stage_embryo="Nori Satoh unpublished cDNA library, cleavage
stage embryo"
/tissue_type="whole animal"
/dev_stage="cleavage stage embryo"
/notes="Vector: pBluescript SK"
BASE COUNT      15 a      5 c      2 g      16 t      1 others
ORIGIN
Query Match      0.9%; Score 21.2; DB 10; Length 39;
Best Local Similarity 88.5%; Pred. No. 3.1e+06;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1743 AATTAACGTGATTTTAAATCA 1768
|||||
Db 31 AATTAACAGTGTATTTTAAATCA 6

RESULT 91
BH235137      39 bp      DNA      linear      GSS 01-JAN-2002
LOCUS      BH235137
DEFINITION      MSAD_E07.x S Spiroplasma kunkelii genomic clone MSAD_E07.x, DNA
ACCESSION      BH235137
VERSION      BH235137.1 GI:18030605
KEYWORDS      GSS.
SOURCE      Spiroplasma kunkelii.
ORGANISM      Spiroplasma kunkelii
Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
Spiroplasmataceae; Spiroplasma.
1 (bases 1 to 39)
REFERENCE      Hogenhout, S.A.
AUTHORS      Genomic sequences from Spiroplasma kunkelii strain M2
TITLE      Unpublished (2001)
JOURNAL      Contact: Hogenhout SA
COMMENT      Department of Entomology
The Ohio State University-OSARD
120 Thorne Hall, 1680 Madison Avenue, Wooster, OH 44691, USA
Tel: 330 263 3730
Fax: 330 263 3686
Email: hogenhout.1@osu.edu
Plate: AD row: E column: 07
Class: shotgun.
Location/Qualifiers
1. .39
/organism="Spiroplasma kunkelii"
/strain="M2"
/db_xref="taxon:47834"
/clone="MSAD_E07.x"
/clone_id="S"
BASE COUNT      14 a      0 c      1 g      24 t
ORIGIN
Query Match      0.9%; Score 21.2; DB 17; Length 39;
Best Local Similarity 76.5%; Pred. No. 3.1e+06;
Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2107 ATCTTTTATATTAATATATTTTCAAT 2140
|||||
Db 1 ATATTTTATATTAATATATTTTATATAT 34

RESULT 92
AA027616      46 bp      mRNA      linear      EST 21-JAN-1997
LOCUS      AA027616
DEFINITION      m108c08.r1 Soares mouse placenta.4NDMP13.5 14.5 Mus musculus cDNA
clone IMAGE:459854.5' similar to SM.SP51_YEAST_P08458
SPORULATION-SPECIFIC PROTEIN 1', mRNA sequence.
AA027616
AA027616.1 GI:1493610
EST.
ACCESSION
VERSION
KEYWORDS

```

```

SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 46)
AUTHORS      Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Gaisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Stepien, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterson, R.
TITLE      The WashU-HMNI Mouse EST Project
JOURNAL      Unpublished (1996)
COMMENT      Contact: Marra M/Mouse EST Project
WashU-HMNI Mouse EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:276742
Possible reversed clone: similarity on wrong strand
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. .46
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:459854"
/clone_id="Soares mouse placenta 4NDMP13.5 14.5"
/sex="unknown"
/tissue_type="placenta"
/dev_stage="adult"
/lab_host="DH10B"
/notes="Organ: Placenta; Vector: pT73D-Pac (Pharmacia)
with a modified polylinker; Site 1: Not I; Site 2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5'
TGTTACCAATCTGAAGTGGAGCGCGCGGAAATTTTATTTTATTTTATTTT
T 3'] ; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Benito Soares and M.Felicia Bonaldo."
BASE COUNT      12 a      8 c      14 g      12 t
ORIGIN
Query Match      0.9%; Score 21.2; DB 9; Length 46;
Best Local Similarity 69.0%; Pred. No. 3.1e+06;
Matches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 778 CACACATTTGTGGACATAGATACATGCGCCCTGAATC 819
|||||
Db 43 CAACCTTTGTGTAAACCATATGTGATGCGCCCTGAATC 2

RESULT 93
BG271415      49 bp      mRNA      linear      EST 20-FEB-2001
LOCUS      BG271415
DEFINITION      na150d11.x1 NCI_CGAP_HN20 Homo sapiens cDNA clone IMAGE:426357 3',
mRNA sequence.
BG271415
BG271415.1 GI:12979533
ACCESSION
VERSION
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE      1 (bases 1 to 49)
AUTHORS      NCI/NIH-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute / National Institute of Dental Research,

```

JOURNAL
COMMENT

Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps@remail.nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL, send email to:
info@image.lln.gov
seq primer: -400P from Glibco.

FEATURES

BASE COUNT	11 a	9 c	9 g	20 t
ORIGIN				

Query Match	0.9%	Score 21.2;	DB 12;	Length 49;
Best Local Similarity	69.0%;	Pred. No. 3.1e+06;		
Matches 29;	Conservative	0;	Mismatches 13;	Indels 0;
				Gaps 0;

Qy 208 CCATATGAACCTGGCATGGAACATGTGAGAAATTTGAATC 245
| | | | | | | | | | | | | | | | | | | | | |
Db 6 CCTATGACATGTTTGTACATCGTTAGAAGCTGAATTC 47

RESULT	94
BG819402	
LOCUS	
DEFINITION	49 bp mRNA linear EST 22-MAY-2001
	BG819402 NC_IGAP_Brn67 Homo sapiens cDNA clone IMAGE:4932703
	5'...mRNA sequence.

FEATURES

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="4932703"
/clone_id="NCI CGAP Brn67"
/tissue_type="anaplastic oligodendroglioma with 1p/19q
loss"
/lab_host="DHIOB (T1 phage-resistant)"
note="Organ: brain; Vector: pCMV-SORT6; Site_1: NCI"

```

BASE COUNT
ORIGIN

Site 2: SalI; cloned unidirectionally. Primer: Oligo dT
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI-CGAP Library."

Query Match	0.9%	Score 21.2;	DB 12;	Length 49;
Best Local Similarity	76.5%;	Pred. No. 3.1e+06;		
Matches	26;	Conservative	0;	Mismatches 8;
			Indels	0;
			Gaps	0;

```

QY 1762 AAATCATCATGTCGCAAAAAAACTTAAG 1795
      ||||| ||||| |||||
Db 16 AAAATCCTCAATTAATCAAAAAAAAG 49

```

RESULT	95
Bj032647	
LOCUS	Bj032647
DEFINITION	51 bp mRNA linear EST 06-DEC-2001
	Bj032647 NIBB Mochizuki normalized Xenopus neurula library Xenopus
	laevis cDNA clone XL017f01 5' mRNA sequence.

FEATURES

SOURCE

Expressed genes in *X. laevis* embryo
Unpublished (2001)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp

BASE COUNT
ORIGIN

18 a	0 c	2 g	29 t	2 others
------	-----	-----	------	----------

Query Match	0.9%	Score 21.2;	DB 13;	Length 51;
Best Local Similarity	72.2%;	Pred. No. 3.1e+06;		
Matches 26; Conservative	0;	Mismatches 10;	Indels 0;	Gaps 0;

Qy	2108	TCTTTTTTTTATATAATATTTTTCCAATAGA	2143
Db	12	TTTTTTTTTTAAATAATTNNNAATTTTTTTAAAAA	47

RESULT	96		
LOCUS	AZ948877/c		
DEFINITION	AZ948877	51 bp	DNA linear GSS 27-APR-2001
ACCESSION	AZ948877		
VERSION	AZ948877.1	GI:13820104	
			Mouse 10kb plasmid UUCGM library Mus musculus genomic clone UUCGM0212P06 F, DNA sequence.

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
SOURCE

GS8.
house mouse.
Mus musculus
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 51)
Dunn, P., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamll, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
'M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0212 ROW: P column: 06
Seq primer: CGTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 51.
Location/Qualifiers
1. 51
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U06C2M0212P06"
/clone_id="Mouse 10kb plasmid U06C2M 1library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g14732114[gblAF129072.1]), a copy-number
inducible derivative of plasmid RL. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
ORIGIN
Query Match 0.9%; Score 21.2; DB 17; Length 51;
Best Local Similarity 64.0%; Pred. No. 3.1e06;
Matches 32; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
Oy 1273 CCATCTGACTTGAAGAAGTGTGAAAAGATTTCTTGAACCAAAAT 1322
Db 50 CCAACTGACTTAAAGAAATACCAATATTTACTTATGCAAGAAATT 1

RESULT 97
AL587783/c 52 bp mRNA linear EST 02-MAR-2001
LOCUS
DEFINITION
R05063B12. mRNA sequence.
ACCESSION
AL587783.1 GI:13192817

KEYWORDS	EST.	
SOURCE	chicken.	
ORGANISM	Gallus gallus	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Archosauria; Aves; Neognathae; Galliformes; Phasianidae;	
	Phasianinae; Gallus.	
REFERENCE	1 (bases 1 to 52)	
AUTHORS	Murray, F.	
TITLE	BP Chicken Brain Library	
JOURNAL	Unpublished (2001)	
COMMENT	Contact: Frazer Murray Dept. Genomics and Bioinformatics Roslin Institute Roslin, Midlothian, EH25 9PS, UK Tel: +44 (0)131 527 4200 Fax: +44 (0)131 440 0434 Email: frazer.murray@bbsrc.ac.uk GGGCGCGCTTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clontech (+6854- Seq primer: M13P.	
FEATURES	Location/Qualifiers	
source	1..52	
	/organism="Gallus gallus"	
	/db_xref="taxon:9031"	
	/clone="ROS063B12"	
	/clone_id="BP Chicken Brain Library"	
	/tissue_type="Brain"	
	/dev_stage="Unknown"	
	/lab_host="DH10B"	
	/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. 5' adaptor sequence: 5' TCGACCTCGAG 3' 3' adaptor sequence: 5' GGGCGCGCTTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clontech (+6854-1)"	
BASE COUNT	9 a 4 c 2 g 37 t	
ORIGIN		
Query Match	0.9%; Score 21.2; DB 9; Length 52;	
Best Local Similarity	69.0%; Pred. No. 3.1e+06;	
Matches	29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	
cy 1761	AAAAATCATCATGTCGCAAAAAAAAAAATTAAGCAATAA 1802	
Db 43	AAAACTATTTAATGGCGCAAAAAAAAAAAAAAAAAAAAA 2	
RESULT 98		
AZ862273	53 bp DNA linear GSS 21-FEB-2001	
LOCUS	AZ862273	
DEFINITION	2M0169H19P Mouse 10kb plasmid UGCM library Mus musculus genomic	
ACCESSION	AZ862273	
VERSION	AZ862273.1 GI:13059411	
KEYWORDS	GSS.	
ORGANISM	house mouse.	
SOURCE	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Rodentia; Scurionath; Muridae; Murine; Mus.	
	1 (bases 1 to 53)	
	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,	
	Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly	
	M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.	
	and Wright, D., Weiss, R.	
	Mouse whole genome scaffolding with paired end reads from 10kb	
	plasmid insects	
	Unpublished (2000)	
	Contact: Robert B. Weiss	
	University of Utah Genome Center	
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT	
	84112, USA	
	Tel: 801 585 5606	
	Fax: 801 585 7177	

Best Local Similarity 76.5%; Pred. No. 3.1e+06;
Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2110 TTTTATATATAATATATATTTTCAATAGA 2143
Db 48 TTGTTAAATAATATAGATTTTAAATAAAA 15

Search completed: April 19, 2003, 10:05:35
Job time : 3729 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2003, 05:16:28 ; Search time 6846 Seconds

(without alignments)
9973.004 Million cell updates/sec

Title: US-09-920-677-3

Perfect score: 2346

Sequence: 1 gcacgagcgtcgcgcggtc.....gtaccacagctcgagacct 2346

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 897812

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

```
GenEmbl:*
1: gb_da:*
2: gb_hcg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_scs:*
28: em_un:*
29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pln:*
35: em_hcg_fod:*
36: em_hcg_mam:*
37: em_hcg_vrt:*
38: em_sy:*
39: em_hcgo_hum:*
40: em_hcgo_mus:*
41: em_hcgo_other:*
```

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25.8	1.1	59	8	S71517 {3, flakin
2	25.6	1.1	51	6	AX203959
3	25	1.1	25	6	AX282921
4	25	1.1	25	6	AX282922
5	24.4	1.0	55	11	AL807848
6	24	1.0	30	6	A48425
7	23.8	1.0	32	6	A48426
8	23.8	1.0	54	6	I08136
9	23.6	1.0	50	6	AX164846
10	23.4	1.0	43	6	AX48439
11	23.4	1.0	54	6	AR002541
12	23.4	1.0	58	6	A51709
13	23.4	1.0	58	6	AR167588
14	23.4	1.0	58	6	AR178298
15	23.4	1.0	58	6	AX323380
16	23	1.0	58	6	A08890
17	22.8	1.0	48	6	AX003947
18	22.8	1.0	48	6	AX021576
19	22.8	1.0	48	6	AX021576
20	22.8	1.0	48	6	AX021632
21	22.6	1.0	51	6	AX115973
22	22.6	1.0	54	6	AR089685
23	22.6	1.0	54	6	AX317217
24	22.4	1.0	44	6	AR032451
25	22.4	1.0	44	6	AR209115
26	22.4	1.0	44	6	I29191
27	22.4	1.0	44	6	I08865
28	22.2	0.9	45	6	AR032600
29	22.2	0.9	45	6	AR209264
30	22.2	0.9	45	6	I29340
31	22.2	0.9	45	6	I91014
32	22.2	0.9	47	6	AX114334
33	22	0.9	33	6	AX172247
34	22	0.9	42	6	AR152463
35	22	0.9	50	6	AX164855
36	22	0.9	58	6	A51710
37	22	0.9	58	6	AR167589
38	22	0.9	58	6	AR178299
39	22	0.9	58	6	AX323381
40	22	0.9	60	6	BD008815
41	21.8	0.9	50	6	AR117934
42	21.8	0.9	50	6	AR117952
43	21.8	0.9	51	6	AX160479
44	21.6	0.9	51	6	AX160117
45	21.6	0.9	51	6	AX160118
46	21.6	0.9	54	9	AF079025
47	21.6	0.9	55	6	AX484751
48	21.4	0.9	31	6	AX248729
49	21.4	0.9	48	6	AR064025
50	21.4	0.9	48	6	AR178317
51	21.4	0.9	48	6	AX323399
52	21.4	0.9	51	6	AX162478
53	21.4	0.9	55	6	I29928
54	21.4	0.9	60	6	I66359
55	21.2	0.9	50	6	AX160974
56	21.2	0.9	51	6	AX157225
57	21.2	0.9	51	6	AX160455
58	21.2	0.9	54	6	AR192747
59	21.2	0.9	54	9	AF254565
60	21.2	0.9	55	6	A43625
61	21.2	0.9	56	6	A80902
62	21.2	0.9	56	6	A87341
63	21.2	0.9	56	6	A97358
64	21.2	0.9	56	6	AR183071
65	21	0.9	38	6	E07494 Synthetic D

c 66 21 0.9 40 6 AX299737 Sequence
67 21 0.9 51 6 AX160105 Sequence
68 21 0.9 56 10 MGSBM24H
69 21 0.9 59 6 AR209950 Sequence
70 21 0.9 59 6 AX253387 Sequence
71 21 0.9 59 6 AX254767 Sequence
72 21 0.9 60 6 AR073297 Sequence
73 21 0.9 60 6 YSCMTP191
74 20.8 0.9 57 3 AF177252 Bodo salt
75 20.6 0.9 28 6 A48423 Sequence 46
76 20.6 0.9 28 6 A48424 Sequence 47
77 20.6 0.9 50 6 A51711 Sequence 17
78 20.6 0.9 50 6 AR167590 Sequence
79 20.6 0.9 50 6 AR178300 Sequence
80 20.6 0.9 50 6 AR165034 Sequence
81 20.6 0.9 50 6 AX323382 Sequence
82 20.6 0.9 51 6 AR068824 Sequence
83 20.6 0.9 51 6 AR122557 Sequence
84 20.6 0.9 51 6 AX157089 Sequence
85 20.6 0.9 51 6 AX157090 Sequence
86 20.6 0.9 51 6 AX158178 Sequence
87 20.6 0.9 51 6 AX161887 Sequence
88 20.6 0.9 51 6 AX161888 Sequence
89 20.6 0.9 51 6 AX162091 Sequence
90 20.6 0.9 51 6 AX162092 Sequence
91 20.6 0.9 53 6 AX404671 Sequence
92 20.6 0.9 54 10 AF328254 Mus muscu
93 20.6 0.9 60 6 E10890 PCR primer
94 20.4 0.9 51 6 AX117117 Sequence
95 20.4 0.9 57 8 YSCMTP182
96 20.2 0.9 39 6 A08918
97 20.2 0.9 45 9 HSU26975 Human iso1a
98 20.2 0.9 48 6 AR032407 Sequence
99 20.2 0.9 48 6 AR209071 Sequence
100 20.2 0.9 48 6 I29147 Sequence 19

ALIGNMENTS

RESULT 1
S71517 59 bp DNA linear PLN 28-OCT-1994
LOCUS {3' flanking DNA of rpl2 exon 2 homolog} [Pisum sativum, Genomic,
59 nt].
S71517
VERSION S71517.1 GI:560660
KEYWORDS
ORGANISM Pisum sativum.
SOURCE Pisum sativum
Pisum sativum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosoid I; Fabales; Fabaceae; Papilionoideae; Viciae;
Pisum.
REFERENCE 1 (bases 1 to 59)
AUTHORS Kocliarova,E.G., Denisenko,Iu.V. and Tarasov,V.A.
TITLE Analysis of nucleotide sequences of 0.7 kb fragments from mixed DNA
from Arabidopsis thaliana and Pisum sativum
JOURNAL Genetics 30 (4), 565-569 (1994)
MEDLINE 94320766
PubMed 8045406
REMARK Genbank staff at the National Library of Medicine created this
entry [NCBI githed 150347] from the original journal article.
This sequence comes from Fig. 2.
FEATURES
source
1..59
Location/Qualifiers
/organism="Pisum sativum"
/db_xref="taxon:3888"
BASE COUNT 16 a 14 c 8 g 21 t
ORIGIN

Query Match 1.1%; Score 25.8; DB 8; Length 59;
Best Local Similarity 67.9%; Pred. No. 2.3e+05;

Matches 36; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
Qy 2134 TTCAATAGATTTTGGATTCAGCTCATTTAGAAACATCCCAACTTAA 2186
Db 3 TTGAAGTAGATTCTTTTATCATTTCAAAACCCCTTCCAAACTGACAA 55

RESULT 2
AX203959 51 bp DNA linear PAT 30-AUG-2001
LOCUS Sequence 65 from Patent WO0148245.
DEFINITION AX203959
ACCESSION AX203959.1 GI:15393422
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimketers,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
method of use thereof
JOURNAL Patent: WO 0148245-A 65 05-JUL-2001;
Curagen Corporation (US)
FEATURES
source
1..51
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
variation
26 /note="single nucleotide polymorphism
Accession number cg4396763"
BASE COUNT 15 a 11 c 6 g 19 t
ORIGIN

Query Match 1.1%; Score 25.6; DB 6; Length 51;
Best Local Similarity 70.8%; Pred. No. 2.5e+05;
Matches 34; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Qy 665 GGATCATCTACAGAGCCGAGCGAGATATATCATGCTTATCACC 712
Db 4 GTATCATCTACCTGTATCTAAAGCTGAAATATCTCTTGTAAAC 51

RESULT 3
AX282921 25 bp DNA linear PAT 02-NOV-2001
LOCUS Sequence 11 from Patent WO0177338.
DEFINITION AX282921
ACCESSION AX282921.1 GI:16609890
VERSION
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Ploewman,G., Whyte,D., Manning,G., Sudarsanam,S., Martinez,R. and
Caenepeel,S.
TITLE Human protein kinases and protein kinase-like enzymes
JOURNAL Patent: WO 0177338-A 11 18-OCT-2001;
Sugen, Inc. (US)
FEATURES
source
1..25
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Primer"

BASE COUNT 10 a 2 c 6 g 7 t
ORIGIN

Query Match 1.1%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.2e+05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 560 GGAACATATTATGACGTTAGAAAG 584
|||||

BASE COUNT 12 a 4 c 5 g 11 t
ORIGIN
Query Match 1.0%; Score 23.8; DB 6; Length 32;
Best Local Similarity 92.6%; Pred. No. 6.3e+05;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1290 TGTGAAGAAAGTTTCTTGAACC 1316
Db 6 TGTGAAGAAAGTTTCTTGAACC 32

RESULT 8
LOCUS 108136 54 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 1 from Patent EP 0343783.
ACCESSION 108136 GI:589151
VERSION 108136.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 54)
AUTHORS Barboiu, J.G.
TITLE Method for producing cells containing stably integrated foreign DNA at a high copy number, the cells produced by this method, and the use of these cells to produce the polypeptides coded for by the foreign DNA
JOURNAL Patent: EP 0343783-A2 1 29-NOV-1989;
FEATURES Location/Qualifiers
source 1..54
/organism="unknown"
BASE COUNT 17 a 0 c 0 g 37 t
ORIGIN

Query Match 1.0%; Score 23.8; DB 6; Length 54;
Best Local Similarity 66.7%; Pred. No. 6.6e+05;
Matches 34; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 2113 TTTTATTAATATATATTTTCAATAGATTTTGATTCGCCATAT 2163
Db 2 TATTTATTTATATATATTTTAAATATATATTTATTTATTTAT 52

RESULT 9
LOCUS AX164846 50 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 41 from Patent WO0138586.
ACCESSION AX164846
VERSION AX164846.1 GI:14545675
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Shinkens, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0138586-A 41 31-MAY-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc_feature 25..26
/note="Nucleotide deleted between bases 25 and 26
Accession number CG4398092"
variation 26
/note="single nucleotide polymorphism"
BASE COUNT 22 a 5 c 3 g 20 t
ORIGIN

Query Match 1.0%; Score 23.6; DB 6; Length 50;
Best Local Similarity 76.3%; Pred. No. 7.3e+05;
Matches 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 2117 TATATTAATATATTTTCAATAGATTTTGATTC 2154
Db 13 TATATTAATATATTTTATTCACAAAATATGTTTATACA 50

RESULT 10
LOCUS AX484399 43 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 1699 from Patent WO02053728.
ACCESSION AX484399
VERSION AX484399.1 GI:22318751
KEYWORDS
SOURCE Candida albicans.
ORGANISM Candida albicans
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE 1
AUTHORS Roemer, T., Jiang, B., Boone, C., Bussey, H. and Olsen, K.L.
TITLE Gene disruption methodologies for drug target discovery
JOURNAL Patent: WO 02053728-A 1699 11-JUN-2002;
Eli Lilly Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
source 1..43
/organism="Candida albicans"
/db_xref="taxon:5476"
BASE COUNT 14 a 4 c 3 g 22 t
ORIGIN

Query Match 1.0%; Score 23.4; DB 6; Length 43;
Best Local Similarity 81.8%; Pred. No. 8e+05;
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2116 TTATATTAATATATTTTCAATAGATTTT 2148
Db 8 TTATATTAATATATTTTCAATAGATTTT 40

RESULT 11
LOCUS AR002541 54 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 72 from patent US 5741696.
ACCESSION AR002541
VERSION AR002541.1 GI:3964095
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 54)
AUTHORS Cochran, M.D. and Chiang, C.H.
TITLE Recombinant equine herpesvirus
JOURNAL Patent: US 5741696-A 72 21-APR-1998;
FEATURES Location/Qualifiers
source 1..54
/organism="unknown"
BASE COUNT 19 a 11 c 8 g 16 t
ORIGIN

Query Match 1.0%; Score 23.4; DB 6; Length 54;
Best Local Similarity 67.3%; Pred. No. 8.2e+05;
Matches 33; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 760 CATGATGAAAGTCAACACACATTTGTGGAACAATAGATCATGG 808
Db 1 CCTATGTATCATACACATACGATTTAGGTGACACTATAGATACCG 49

RESULT 12
LOCUS AS1709 58 bp DNA linear PAT 10-MAR-1997

DEFINITION Sequence 15 from Patent WO9618744.
ACCESSION A51709
VERSION A51709.1 GI:2304513
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 58)
AUTHORS Crouzet,J., Scherman,D. and Wils,P.
TITLE PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN IMMOBILIZED OLIGONUCLEOTIDE
JOURNAL Patent: WO 9618744-A 15 20-JUN-1996;
Rhone Poulenc Korer SA (FR)
COMMENT Other publication AU 4178996 960703
Other publication FR 2728264 960621.
FEATURES Location/Qualifiers
source 1..58
/organism="unclassified"
/db_xref="taxon:32644"
BASE COUNT 18 a 2 c 37 g 1 t
ORIGIN

Query Match 1.0%; Score 23.4; DB 6; Length 58;
Best Local Similarity 63.2%; Pred. No. 8.2e+05;
Matches 36; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 118 GACCTGGACACGACGAGGAGCGGGCTCTGAGATGAGCTGGAGAGGGGGGTCTAG 174
Db 1 GATCCGAG 57

RESULT 13
LOCUS ARI67588 58 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 15 from patent US 6287762.
ACCESSION ARI67588
VERSION ARI67588.1 GI:17903377
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 58)
AUTHORS Crouzet,J., Scherman,D. and Wils,P.
TITLE Purification of a triple helix formation with an immobilized oligonucleotide
JOURNAL Patent: US 6287762-A 15 11-SEP-2001;
FEATURES Location/Qualifiers
source 1..58
/organism="unknown"
BASE COUNT 18 a 2 c 37 g 1 t
ORIGIN

Query Match 1.0%; Score 23.4; DB 6; Length 58;
Best Local Similarity 63.2%; Pred. No. 8.2e+05;
Matches 36; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 118 GACCTGGACACGACGAGGAGCGGGCTCTGAGATGAGCTGGAGAGGGGGGTCTAG 174
Db 1 GATCCGAG 57

RESULT 14
LOCUS ARI78298 58 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 15 from patent US 6319672.
ACCESSION ARI78298
VERSION ARI78298.1 GI:20219436
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 58)
AUTHORS Crouzet,J., Scherman,D., Wils,P., Blanche,F. and Cameron,B.

TITLE Purification of a triple helix formation with an immobilized oligonucleotide
JOURNAL Patent: US 6319672-A 15 20-NOV-2001;
FEATURES Location/Qualifiers
source 1..58
/organism="unknown"
BASE COUNT 18 a 2 c 37 g 1 t
ORIGIN

Query Match 1.0%; Score 23.4; DB 6; Length 58;
Best Local Similarity 63.2%; Pred. No. 8.2e+05;
Matches 36; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 118 GACCTGGACACGACGAGGAGCGGGCTCTGAGATGAGCTGGAGAGGGGGGTCTAG 174
Db 1 GATCCGAG 57

RESULT 15
LOCUS AX323380 58 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 15 from Patent WO0192511.
ACCESSION AX323380
VERSION AX323380.1 GI:18094142
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Crouzet,J., Scherman,D., Wils,P., Blanche,F. and Cameron,B.
TITLE Purification of a triple helix formation with an immobilized oligonucleotide
JOURNAL Patent: WO 0192511-A 15 06-DEC-2001;
Aventis Pharma (FR)
FEATURES Location/Qualifiers
source 1..58
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
BASE COUNT 18 a 2 c 37 g 1 t
ORIGIN

Query Match 1.0%; Score 23.4; DB 6; Length 58;
Best Local Similarity 63.2%; Pred. No. 8.2e+05;
Matches 36; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 118 GACCTGGACACGACGAGGAGCGGGCTCTGAGATGAGCTGGAGAGGGGGGTCTAG 174
Db 1 GATCCGAG 57

RESULT 16
LOCUS A08890 58 bp DNA linear PAT 02-SEP-1993
DEFINITION H.sapiens (haplotype 1, allele MS32, isolate French, serial number 6) minisatellite sequence.
ACCESSION A08890
VERSION A08890.1 GI:411812
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 58)
AUTHORS Jeffreys,A.J.
TITLE Extended nucleotide sequences
JOURNAL Patent: EP 0370719-A 70 30-MAY-1990;
IMPERIAL CHEMICAL INDUSTRIES PLC
FEATURES Location/Qualifiers
source 1..58
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 34 a 0 c 0 g 24 t

ACCESSION AX115973
VERSION AX115973.1 GI:14032915
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Picoult-Newburg, L. and Pohl, M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 1096 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES
source
1..51
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 13 a 9 c 8 g 20 t 1 others
ORIGIN

Query Match 1.0%; Score 22.6; DB 6; Length 51;
Best Local Similarity 68.9%; Pred. No. 1.2e+06;
Matches 31; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 406 AGCGAATGATGCTAAGAAATGCTAAGATACAGCTCATACAAA 450
DB 51 ATGGCAATGATATTCAGACATTCATACGATATATCTGTGAAAA 7

RESULT 22
AR089685 AR089685 54 bp DNA linear PAT 07-SEP-2000
LOCUS
DEFINITION Sequence 162 from patent US 5994069.
ACCESSION AR089685
VERSION AR089685.1 GI:10016440
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 54)
AUTHORS Hall, J.G., Lyamichev, V.I., Mast, A.L. and Brow, M. Ann.D.
TITLE Detection of nucleic acids by multiple sequential invasive
cleavages
JOURNAL Patent: US 5994069-A 162 30-NOV-1999;
FEATURES
source
1..54
/organism="unknown"
BASE COUNT 14 a 7 c 25 g 8 t
ORIGIN

Query Match 1.0%; Score 22.6; DB 6; Length 54;
Best Local Similarity 75.7%; Pred. No. 1.3e+06;
Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 128 AGCCAGAGAGACCGGGCTCTGAGATGAGCTGAGAGA 164
DB 4 AGGAAGAGAGAGAGAGGGTCTCAGAGAGAGCGGAGAGA 40

RESULT 23
AX317217 AX317217 54 bp DNA linear PAT 14-DEC-2001
LOCUS
DEFINITION Sequence 220 from Patent WO0190337.
ACCESSION AX317217
VERSION AX317217.1 GI:17900206
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Allawi, H., Bartholomay, C.T., Chehak, L., Curtis, M.L., Eis, P.S.,
Hall, J.G., Ip, H.S., Kaiser, M., Kwiatkowski, R.W., Lukowiak, A.A.,
Lyamichev, V., Ma, W., Olson-Munoz, M.C., Olson, S.M., Schaefer, J.U.,
Skizypeczynski, Z., Takova, T.Y., Vedvik, K.L. and Lyamichev, N.B.

TITLE Detection of rna
JOURNAL Patent: WO 0190337-A 220 29-NOV-2001;
THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES
source
1..54
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 14 a 7 c 25 g 8 t
ORIGIN

Query Match 1.0%; Score 22.6; DB 6; Length 54;
Best Local Similarity 75.7%; Pred. No. 1.3e+06;
Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 128 AGCCAGAGAGACCGGGCTCTGAGATGAGCTGAGAGA 164
DB 4 AGGAAGAGAGAGAGAGGGTCTCAGAGAGAGCGGAGAGA 40

RESULT 24
AR032451 AR032451 44 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 63 from patent US 5869241.
ACCESSION AR032451
VERSION AR032451.1 GI:5948056
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 44)
AUTHORS Edwards, C.A., Cantor, C.R., Andrews, B.M., Turin, L.M. and Fry, K.E.
TITLE Method of determining DNA sequence preference of a DNA-binding
molecule
JOURNAL Patent: US 5869241-A 63 09-FEB-1999;
FEATURES
source
1..44
/organism="unknown"
BASE COUNT 6 a 15 c 20 g 3 t
ORIGIN

Query Match 1.0%; Score 22.4; DB 6; Length 44;
Best Local Similarity 72.5%; Pred. No. 1.4e+06;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 9 CTGCGCGGGTCCGGCCCATGAGCGGAGAGAGCGG 48
DB 4 CTCGCCGAGCGCGGCGCATATGAGAGGCGGCGCGG 43

RESULT 25
AR209115 AR209115 44 bp DNA linear PAT 20-JUN-2002
LOCUS
DEFINITION Sequence 63 from patent US 6384208.
ACCESSION AR209115
VERSION AR209115.1 GI:21510447
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 44)
AUTHORS Edwards, C.A., Cantor, C.R., Andrews, B.M., Turin, L.M. and Fry, K.E.
TITLE Sequence directed DNA binding molecules compositions and methods
JOURNAL Patent: US 6384208-A 63 07-MAY-2002;
FEATURES
source
1..44
/organism="unknown"
BASE COUNT 6 a 15 c 20 g 3 t
ORIGIN

Query Match 1.0%; Score 22.4; DB 6; Length 44;
Best Local Similarity 72.5%; Pred. No. 1.4e+06;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 9 CTGCGCGGCTCCGGCCCATGAGCGGAGGAGGCGG 48
Db 4 CTGCGCGGAGCGGCGCATATGAGGAGGAGGCGGCGG 43

RESULT 26

LOCUS 129191 44 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 63 from patent US 5578444.
ACCESSION 129191
VERSION 129191.1 GI:1819982
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 44)
AUTHORS Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
TITLE Sequence-directed DNA-binding molecules compositions and methods
JOURNAL Patent: US 5578444-A 63 26-NOV-1996;
FEATURES Location/Qualifiers
source 1..44
/organism="unknown"

BASE COUNT 6 a 15 c 20 g 3 t

Query Match 1.0%; Score 22.4; DB 6; Length 44;
Best Local Similarity 72.5%; Pred. No. 1.4e+06;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 9 CTGCGCGGCTCCGGCCCATGAGCGGAGGAGGCGG 48
Db 4 CTGCGCGGAGCGGCGCATATGAGGAGGAGGCGGCGG 43

RESULT 27

LOCUS 190865 44 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 63 from patent US 5726014.
ACCESSION 190865
VERSION 190865.1 GI:3935335
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 44)
AUTHORS Edwards,C.A., Cantor,C.R., Andrews,B.M. and Turin,L.M.
TITLE Screening assay for the detection of DNA-binding molecules
JOURNAL Patent: US 5726014-A 63 10-MAR-1998;
FEATURES Location/Qualifiers
source 1..44
/organism="unknown"

BASE COUNT 6 a 15 c 20 g 3 t

Query Match 1.0%; Score 22.4; DB 6; Length 44;
Best Local Similarity 72.5%; Pred. No. 1.4e+06;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 9 CTGCGCGGCTCCGGCCCATGAGCGGAGGAGGCGG 48
Db 4 CTGCGCGGAGCGGCGCATATGAGGAGGAGGCGGCGG 43

RESULT 28

LOCUS AR032600 45 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 212 from patent US 5869241.
ACCESSION AR032600
VERSION AR032600.1 GI:5948205
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 45)
AUTHORS Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
TITLE Method of determining DNA sequence preference of a DNA-binding molecule
JOURNAL Patent: US 5869241-A 212 09-FEB-1999;
FEATURES Location/Qualifiers
source 1..45
/organism="unknown"

BASE COUNT 13 a 10 c 7 g 15 t

Query Match 0.9%; Score 22.2; DB 6; Length 45;
Best Local Similarity 77.1%; Pred. No. 1.5e+06;
Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 933 TGACAAATTCCTCAATGTAACTCAATTTGCCTC 967
Db 9 TAAACGAAATTTCCATGTAACTCAATTTCCCTC 43

RESULT 29

LOCUS AR209264 45 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 212 from patent US 6384208.
ACCESSION AR209264
VERSION AR209264.1 GI:21510637
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 45)
AUTHORS Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
TITLE Sequence directed DNA binding molecules compositions and methods
JOURNAL Patent: US 6384208-A 212 07-MAY-2002;
FEATURES Location/Qualifiers
source 1..45
/organism="unknown"

BASE COUNT 13 a 10 c 7 g 15 t

Query Match 0.9%; Score 22.2; DB 6; Length 45;
Best Local Similarity 77.1%; Pred. No. 1.5e+06;
Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 933 TGACAAATTCCTCAATGTAACTCAATTTGCCTC 967
Db 9 TAAACGAAATTTCCATGTAACTCAATTTCCCTC 43

RESULT 30

LOCUS 129340 45 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 212 from patent US 5578444.
ACCESSION 129340
VERSION 129340.1 GI:1820131
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 45)
AUTHORS Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
TITLE Sequence-directed DNA-binding molecules compositions and methods
JOURNAL Patent: US 5578444-A 212 26-NOV-1996;
FEATURES Location/Qualifiers
source 1..45
/organism="unknown"

BASE COUNT 13 a 10 c 7 g 15 t

Query Match 0.9%; Score 22.2; DB 6; Length 45;
Best Local Similarity 77.1%; Pred. No. 1.5e+06;
Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY	933	TGACAAATTCCTCAATGTAAATCAATTGCCTC	967
Db	9	TAAAGAAAATTCCATGTAACTCATTTTCCCTC	43
RESULT	31		
LOCUS	191014	45 bp	DNA
DEFINITION	Sequence 212 from patent US 5726014.		linear
ACCESSION	191014		PAT 01-DEC-1998
VERSION	191014.1	GI:3935484	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 45)		
AUTHORS	Edward,C.A., Cantor,C.R., Andrews,B.M. and Turin,L.M.		
TITLE	Screening assay for the detection of DNA-binding molecules		
JOURNAL	Patent: US 5726014-A 212 10-MAR-1998;		
FEATURES	Location/Qualifiers		
source	1..45		
BASE COUNT	13 a 10 c 7 g 15 t		
ORIGIN	/organism="unknown"		
Query Match	0.9%; Score 22.2; DB 6;	Length 45;	
Best Local Similarity	77.1%; Pred. No. 1.5e+06;		
Matches	27; Conservative 0; Mismatches 8;	Indels 0;	Gaps 0;
OY	933	TGACAAATTCCTCAATGTAACTCAATTGGCTC	967
Db	9	TAAAGAAAATTCCATGTAACTCATTTTCCCTC	43
RESULT	32		
LOCUS	AX114334/c	47 bp	DNA
DEFINITION	Sequence 3 from Patent WO0129257.		linear
ACCESSION	AX114334		PAT 11-MAY-2001
VERSION	AX114334.1	GI:14031298	
KEYWORDS	.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 47) Schork,N. and Skierczynski,B. Methods of genetic cluster analysis and use thereof Patent: WO 0129257-A 3 26-APR-2001;		
TITLE	GENSET (FR)		
JOURNAL	Location/Qualifiers		
FEATURES	1..47		
source	/organism="Homo sapiens" /db_xref="taxon:9606" 24		
variation	/note="10-88-81 : polymorphic base C or T" 24		
BASE COUNT	23 a 6 c 5 g 12 t		
ORIGIN	1 others		
Query Match	0.9%; Score 22.2; DB 6;	Length 47;	
Best Local Similarity	66.7%; Pred. No. 1.5e+06;		
Matches	30; Conservative 1; Mismatches 14;	Indels 0;	Gaps 0;
OY	2107	ATCTTTTTTTATATAATATATATTTTCAATAGATTTTGAT	2151
Db	47	AGTTTGGTTGAATTCACATAGATTTCAGTTAATCTTAAT	3
RESULT	33		
LOCUS	AX172247/c	33 bp	DNA
DEFINITION	Sequence 30 from Patent WO0144497.		linear
ACCESSION	AX172247		PAT 03-JUL-2001

VERSION	AXI72247.1	GI:14597474
KEYWORDS		
SOURCE	synthetic construct.	
ORGANISM	synthetic construct artificial sequences.	
REFERENCE	1 (bases 1 to 33)	
AUTHORS	Alesci,D. and Biondi,R.	
TITLE	Protein kinase regulation	
JOURNAL	Patent: WO 014497-A 30 21-JUN-2001, The University of Dundee (GB)	
FEATURES	Location/Qualifiers	
source	1..33 /organism="synthetic construct" /db_xref="taxon:32630" /note="PCR primer"	
BASE COUNT	8 a	9 g 6 t
ORIGIN		
Query Match	0.9%; Score 22;	DB 6; Length 33;
Best Local Similarity	100.0%;	Pred. No. 1.7e+06;
Matches	22; Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
Oy	1269 GGCTCCATCTGACTTGAAGT	1290
Db	33 GGCTCATCTGTACTTGAAAGT	12
RESULT 34		
LOCUS	ARI52463	42 bp DNA linear PAT 08-AUG-2001
DEFINITION	Sequence 31 from patent US 6235263.	
ACCESSION	ARI52463	
VERSION	ARI52463.1	GI:15119995
KEYWORDS	Unknown.	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 42)	
AUTHORS	Wong,A.K.C., Bartel,P.L., Teng,D.H.-F. and Tavligian,S.V.	
TITLE	Carboxy-terminal BRCA1 interacting protein	
JOURNAL	Patent: US 6235263-A 31 22-MAY-2001;	
FEATURES	Location/Qualifiers	
source	1..42 /organism="unknown"	
BASE COUNT	15 a	11 c 10 g 6 t
ORIGIN		
Query Match	0.9%; Score 22;	DB 6; Length 42;
Best Local Similarity	73.7%;	Pred. No. 1.7e+06;
Matches	28; Conservative 0;	Mismatches 10; Indels 0; Gaps 0;
Oy	2034 TTTTCCGAGCGAAATGGGAGGCACAAGAACA	2071
Db	2 TTTTCCAGTCACGCGGAGGAAATCACAAGAACA	39
RESULT 35		
LOCUS	AXI64855/C	50 bp DNA linear PAT 22-JUN-2001
DEFINITION	Sequence 50 from Patent WO0138586.	
ACCESSION	AXI64855	
VERSION	AXI64855.1	GI:14545684
KEYWORDS	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 50) Shinketsu,R.A. and Leach,M. Nucleic acids containing single nucleotide polymorphisms and methods of use thereof Patent: WO 0138586-A 50 31-MAY-2001; Curagen Corporation (US)	
TITLE		
JOURNAL		

FEATURES Location/Qualifiers
source 1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc_feature 25..26
/note="Nucleotide deleted between bases 25 and 26
Accession number CG43056971"
variation 26
/note="single nucleotide polymorphism"
BASE COUNT 16 a 4 c 8 g 22 t
ORIGIN

Query Match 0.9%; Score 22; DB 6; Length 50;
Best Local Similarity 67.4%; Pred. No. 1.7e+06;
Matches 31; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 2096 AAGACCTGATCTTTTATATAATATATTTTCAATA 2141
Db 48 AAGACCTTTTACACACTTGGAAAAATAGGATTTTCAATA 3

RESULT 36
AS1710/c AS1710 58 bp DNA linear PAT 10-MAR-1997
LOCUS Sequence 16 from Patent WO9618744.
DEFINITION AS1710
ACCESSION AS1710
VERSION AS1710.1 GI:2304514
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 58)
AUTHORS Crouzet,J., Sherman,D. and Wils,P.
TITLE PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN IMMOBILIZED OLIGONUCLEOTIDE
JOURNAL Patente: WO 9618744-A 16 20-JUN-1996;
Rhone Poulenc Rorer SA (FR)
COMMENT Other publication AU 417896 960703
Other publication FR 2728264 960621.
FEATURES Location/Qualifiers
source 1..58
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 2 a 36 c 1 g 19 t
ORIGIN

Query Match 0.9%; Score 22; DB 6; Length 58;
Best Local Similarity 63.0%; Pred. No. 1.7e+06;
Matches 34; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 123 GGACGACGACGAGGAGCGGCTCTGAGATGAGCTGAGAGGAGGAGTCAATT 176
Db 54 GGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAAATT 1

RESULT 37
AR167589/c AR167589 58 bp DNA linear PAT 17-DEC-2001
LOCUS Sequence 16 from patent US 6287762.
DEFINITION AR167589
ACCESSION AR167589
VERSION AR167589.1 GI:17903378
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 58)
AUTHORS Crouzet,J., Sherman,D. and Wils,P.
TITLE Purification of a triple helix formation with an immobilized oligonucleotide
JOURNAL Patent: US 6287762-A 16 11-SEP-2001;
FEATURES Location/Qualifiers
source 1..58
/organism="unknown"

BASE COUNT 2 a 36 c 1 g 19 t
ORIGIN

Query Match 0.9%; Score 22; DB 6; Length 58;
Best Local Similarity 63.0%; Pred. No. 1.7e+06;
Matches 34; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 123 GGACGACGACGAGGAGCGGCTCTGAGATGAGCTGAGAGGAGGAGTCAATT 176
Db 54 GGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAAATT 1

RESULT 38
AR178299/c AR178299 58 bp DNA linear PAT 20-APR-2002
LOCUS Sequence 16 from patent US 6319672.
DEFINITION AR178299
ACCESSION AR178299
VERSION AR178299.1 GI:20219437
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 58)
AUTHORS Crouzet,J., Sherman,D., Wils,P., Blanche,F. and Cameron,B.
TITLE Purification of a triple helix formation with an immobilized oligonucleotide
JOURNAL Patent: US 6319672-A 16 20-NOV-2001;
FEATURES Location/Qualifiers
source 1..58
/organism="unknown"
BASE COUNT 2 a 36 c 1 g 19 t
ORIGIN

Query Match 0.9%; Score 22; DB 6; Length 58;
Best Local Similarity 63.0%; Pred. No. 1.7e+06;
Matches 34; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 123 GGACGACGACGAGGAGCGGCTCTGAGATGAGCTGAGAGGAGGAGTCAATT 176
Db 54 GGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAAATT 1

RESULT 39
AX323381/c AX323381 58 bp DNA linear PAT 07-JAN-2002
LOCUS Sequence 16 from Patent WO0192511.
DEFINITION AX323381
ACCESSION AX323381
VERSION AX323381.1 GI:18094143
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Crouzet,J., Sherman,D., Wils,P., Blanche,F. and Cameron,B.
TITLE Purification of a triple helix formation with an immobilized oligonucleotide
JOURNAL Patent: WO 0192511-A 16 06-DEC-2001;
Aventis Pharma (FR)
FEATURES Location/Qualifiers
source 1..58
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
BASE COUNT 2 a 36 c 1 g 19 t
ORIGIN

Query Match 0.9%; Score 22; DB 6; Length 58;
Best Local Similarity 63.0%; Pred. No. 1.7e+06;
Matches 34; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 123 GGACGACGACGAGGAGCGGCTCTGAGATGAGCTGAGAGGAGGAGTCAATT 176
Db 54 GGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAAATT 1

RESULT 40
BD008815 60 bp DNA linear PAT 31-JAN-2002
LOCUS Adhesin binding group antigen.
DEFINITION BD008815
ACCESSION BD008815.1 GI:18637188
VERSION JP 2001503606-A/3.
KEYWORDS Helicobacter pylori.
SOURCE Helicobacter pylori
ORGANISM Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group; Helicobacter.
REFERENCE 1 (bases 1 to 60)
AUTHORS Boren,T., Arngqvist,A., Normark,S., Ilver,D. and Hammarstrom,L.
TITLE Adhesin binding group antigen
JOURNAL Patent: JP 2001503606-A 3 21-MAR-2001;
THOMAS BOREN
COMMENT OS Helicobacter pylori
PN JP 2001503606-A/3
PD 21-MAR-2001
PR 10-JUN-1997 JP 1998501515
PT THOMAS BOREN,ANNA ARNGVIST,STAFFAN NORMARK,DAG ILLVER, PI LENNART HAMMARSTROM
PC C07K14/205,A61K39/106,C07K16/12
CC
FH Key location/Qualifiers
FT source /organism='Helicobacter pylori'.
FEATURES
source location/Qualifiers
1..60
/organism='Helicobacter pylori'
/db_xref='taxon:210'
BASE COUNT 19 a 13 c 16 g 12 t
ORIGIN
Query Match 0.9%; Score 22; DB 6; Length 60;
Best Local Similarity 63.0%; Pred. No. 1.7e+06;
Matches 34; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
Qy 49 GACGGCTTTTACCCAGCCCGGACTTCGAGACGAGGAGCTGAGACATGGCA 102
Db 7 GACGGCTTTTACCAACGATGAGCTATCAAAATCGGTGAGACCGCTCAATGGTA 60
RESULT 41
AR117934/c 50 bp DNA linear PAT 16-MAY-2001
LOCUS AR117934
DEFINITION Sequence 7 from patent US 6140470.
ACCESSION AR117934
VERSION AR117934.1 GI:14098840
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 50)
AUTHORS Garen,A. and Cai,X.
TITLE Human monoclonal anti-tumor antibodies
JOURNAL Patent: US 6140470-A 7 31-OCT-2000;
FEATURES Location/Qualifiers
source 1..50
/organism='unknown'
BASE COUNT 6 a 11 c 20 g 10 t 3 others
ORIGIN
Query Match 0.9%; Score 21.8; DB 6; Length 50;
Best Local Similarity 67.4%; Pred. No. 1.9e+06;
Matches 29; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
Qy 1501 GCATCGGACACCACTTCATAGACAGCCGGAAGTCTGGGCGCAT 1543
Db 43 SCAMCAGCTGCACCTCGGCGCACGTGGCGGAAACCTGAGCCAT 1

RESULT 42
AR117952/c 50 bp DNA linear PAT 16-MAY-2001
LOCUS AR117952
DEFINITION Sequence 44 from patent US 6140470.
ACCESSION AR117952
VERSION AR117952.1 GI:14098858
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 50)
AUTHORS Garen,A. and Cai,X.
TITLE Human monoclonal anti-tumor antibodies
JOURNAL Patent: US 6140470-A 44 31-OCT-2000;
FEATURES Location/Qualifiers
source 1..50
/organism='unknown'
BASE COUNT 6 a 11 c 20 g 10 t 3 others
ORIGIN
Query Match 0.9%; Score 21.8; DB 6; Length 50;
Best Local Similarity 67.4%; Pred. No. 1.9e+06;
Matches 29; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
Qy 1501 GCATCGGACACCACTTCATAGACAGCCGGAAGTCTGGGCGCAT 1543
Db 43 SCAMCAGCTGCACCTCGGCGCACGTGGCGGAAACCTGAGCCAT 1
RESULT 43
AX160479 51 bp DNA linear PAT 22-JUN-2001
LOCUS AX160479
DEFINITION Sequence 3807 from Patent WO0140521.
ACCESSION AX160479
VERSION AX160479.1 GI:14541810
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 51)
AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Shmkeets,R.A. and Leach,M.
JOURNAL Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
Patent: WO 0140521-A 3807 07-JUN-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..51
/organism='Homo sapiens'
misc_feature /db_xref='taxon:9606'
26
/note='1 of 2 allelic variants (3808 is other entry)
Accession number CG43920546'
BASE COUNT 33 a 9 c 5 g 4 t
ORIGIN
Query Match 0.9%; Score 21.8; DB 6; Length 51;
Best Local Similarity 70.7%; Pred. No. 1.9e+06;
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Qy 918 TAGAAGAAAACAATTGACAAATCTCAAAATGTAACCTCA 958
Db 10 TAGAAGAAAACAATAAACAACCACTCAAGAGAAAACA 50
RESULT 44
AX160117/c 51 bp DNA linear PAT 22-JUN-2001
LOCUS AX160117
DEFINITION Sequence 3445 from Patent WO0140521.
ACCESSION AX160117
VERSION AX160117.1 GI:14541448

KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE 1 (bases 1 to 51)
JOURNAL Nucleic acids containing single nucleotide polymorphisms and
AUTHORS Shinkens,R.A. and Leach,M.
TITLE Methods of use thereof
JOURNAL Patent: WO 0140521-A 3445 07-JUN-2001;
Curation Corporation (US)
FEATURES
SOURCE Location/Qualifiers
misc_feature
/note="1 of 2 allelic variants (3446 is other entry)"
/db_xref="taxon:9606"
BASE COUNT 13 a 10 c 5 g 23 t
ORIGIN

Query Match 0.9%; Score 21.6; DB 6; Length 51;
Best Local Similarity 68.2%; Pred. No. 2.1e+06;
Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1278 TGTACTTGAAGTGTGAAGAAAGTTTCCTTGAACCAAAA 1321
DB 45 TGTACACTAAATGTGAAGTTTGTAAAAAGAAAA 2

RESULT 45
LOCUS AX160118 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 3446 from Patent WO0140521.
ACCESSION AX160118
VERSION AX160118.1 GI:14541449
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE 1 (bases 1 to 51)
JOURNAL Nucleic acids containing single nucleotide polymorphisms and
AUTHORS Shinkens,R.A. and Leach,M.
TITLE Methods of use thereof
JOURNAL Patent: WO 0140521-A 3446 07-JUN-2001;
Curation Corporation (US)
FEATURES
SOURCE Location/Qualifiers
misc_feature
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="2 of 2 allelic variants (3445 is other entry)"
Accession number CG43271689"
BASE COUNT 12 a 10 c 6 g 23 t
ORIGIN

Query Match 0.9%; Score 21.6; DB 6; Length 51;
Best Local Similarity 68.2%; Pred. No. 2.1e+06;
Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1278 TGTACTTGAAGTGTGAAGAAAGTTTCCTTGAACCAAAA 1321
DB 45 TGTACACTAAATGTGAAGTTTGTAAAAAGAAAA 2

RESULT 46
LOCUS AF079025/c 54 bp mRNA linear PRI 15-SEP-1999
DEFINITION Homo sapiens clone AV22-1 T-cell receptor alpha chain (TCRA) mRNA,
partial cds.
ACCESSION AF079025
VERSION AF079025.1 GI:5881986

KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE 1 (bases 1 to 54)
JOURNAL Fontenot,A.P., Falta,M.T., Newman,L.S. and Kotzin,B.L.
AUTHORS Identification of pathogenic T-cells in patients with
TITLE beryllium-induced lung disease
JOURNAL Unpublished
REFERENCE
AUTHORS 2 (bases 1 to 54)
TITLE Fontenot,A.P., Falta,M.T., Newman,L.S. and Kotzin,B.L.
JOURNAL Direct Submission
TITLE Submitted (15-JUL-1998) Medicine and Pediatrics, National Jewish
JOURNAL Medical and Research Center, 1400 Jackson Street, K1020, Denver, CO
80206, USA
FEATURES
SOURCE Location/Qualifiers
misc_feature
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="AV22-1"
/cell_type="CD4+"
/note="Isolated from peripheral blood and bronchoalveolar
lavage of patient 2 with chronic beryllium disease"
<1..>54
/gene="TCRA"
<1..>54
/gene="CDR3; 3' end of TCRAV22 to 5' end of AJ8"
/note="CDR3; 3' end of TCRAV22 to 5' end of AJ8"
/codon_start=1
/product="T-cell receptor alpha chain"
/protein_id="AAD5151.1"
/db_xref="GI:5882002"
/translation="VYFCALSDNMGFKLVFG"
BASE COUNT 13 a 9 c 13 g 19 t
ORIGIN

Query Match 0.9%; Score 21.6; DB 9; Length 54;
Best Local Similarity 68.2%; Pred. No. 2.1e+06;
Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1685 TCATAATGACAGTTTCAGAGATCATGTCTATCATATGAACAC 1728
DB 54 TCCTAATGCAAGTTCTGAAGCCGTGTATCACTGACAGAC 11

RESULT 47
LOCUS AX484751 55 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 2051 from Patent WO02053728.
ACCESSION AX484751
VERSION AX484751.1 GI:22319035
KEYWORDS
SOURCE Candida albicans.
ORGANISM Candida albicans
REFERENCE
AUTHORS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
TITLE Saccharomycetales; mitosporic Saccharomycetales; Candida.
JOURNAL Rosmer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.
TITLE Gene disruption methodologies for drug target discovery
JOURNAL Patent: WO 02053728-A 2051 11-JUL-2002;
Eliara Pharmaceuticals, Inc. (US)
FEATURES
SOURCE Location/Qualifiers
misc_feature
/organism="Candida albicans"
/db_xref="taxon:5476"
BASE COUNT 12 a 9 c 25 t
ORIGIN

Query Match 0.9%; Score 21.6; DB 6; Length 55;
Best Local Similarity 68.2%; Pred. No. 2.1e+06;
Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 913 GAGAAATAGAAAGAAACAAATTGACAAATCTCAAAATGTAACCT 956
Db 45 GGGGAGAAAAAGAAACAAATATGACAAATCACTCACTTAATT 2

RESULT 48
AX248729 31 bp DNA linear PAT 28-SEP-2001
LOCUS AX248729
DEFINITION Sequence 808 from Patent WO0166800.
ACCESSION AX248729
VERSION AX248729.1 GI:15863352
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
AUTHORS 1 (bases 1 to 31)
TITLE Cargili, M., Ireland, J.S. and Landier, E.S.
JOURNAL Human single nucleotide polymorphisms
PATENT: WO 0166800-A 808 13-SEP-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)

FEATURES
Location/Qualifiers
1..31
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 14 a 5 c 4 g 7 t 1 others
ORIGIN

Query Match 0.9%; Score 21.4; DB 6; Length 31;
Best Local Similarity 88.0%; Pred. No. 2.3e+06;
Matches 22; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1777 TGCAGAAAAAACTTAAGCAAAAT 1801
Db 6 TCCAAAAAARACTTACGCAAAAT 30

RESULT 49
AR064025 48 bp DNA linear PAT 29-SEP-1999
LOCUS AR064025
DEFINITION Sequence 12 from patent US 5846774.
ACCESSION AR064025
VERSION AR064025.1 GI:5993333
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 48)
AUTHORS Xia, Y.
TITLE Chlorella virus promoters
JOURNAL Patent: US 5846774-A 12 08-DEC-1998;
FEATURES Location/Qualifiers
1..48
/organism="unknown"

BASE COUNT 17 a 7 c 9 g 15 t
ORIGIN

Query Match 0.9%; Score 21.4; DB 6; Length 48;
Best Local Similarity 66.0%; Pred. No. 2.4e+06;
Matches 31; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 2233 CTTCTCTTGTAATTAATGCAATGATCATTTGTTAACA 2279
Db 2 CTTATCGTGTATGATTAATGACAAATGATACGCTGATCAACA 48

RESULT 50
AR178317 48 bp DNA linear PAT 20-APR-2002
LOCUS AR178317
DEFINITION Sequence 34 from patent US 6319672.
ACCESSION AR178317
VERSION AR178317.1 GI:20219455
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 48)
AUTHORS Crouzet, J., Scherman, D., Wils, P., Blanche, F. and Cameron, B.
TITLE Purification of a triple helix formation with an immobilized oligonucleotide
JOURNAL Patent: US 6319672-A 34 20-NOV-2001;
FEATURES Location/Qualifiers
1..48
/organism="unknown"

BASE COUNT 16 a 0 c 32 g 0 t
ORIGIN

Query Match 0.9%; Score 21.4; DB 6; Length 48;
Best Local Similarity 66.0%; Pred. No. 2.4e+06;
Matches 31; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 123 GGACGAGCCAGAGAGCGGGCTTGAGAGTACGCTGAGAGGGGG 169
Db 1 GGAGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGG 47

RESULT 51
AX323399 48 bp DNA linear PAT 07-JAN-2002
LOCUS AX323399
DEFINITION Sequence 34 from Patent WO0192511.
ACCESSION AX323399
VERSION AX323399.1 GI:18094161
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Crouzet, J., Scherman, D., Wils, P., Blanche, F. and Cameron, B.
TITLE Purification of a triple helix formation with an immobilized oligonucleotide
JOURNAL Patent: WO 0192511-A 34 06-DEC-2001;
Aventis Pharma (FR)

FEATURES
Location/Qualifiers
1..48
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

BASE COUNT 16 a 0 c 32 g 0 t
ORIGIN

Query Match 0.9%; Score 21.4; DB 6; Length 48;
Best Local Similarity 66.0%; Pred. No. 2.4e+06;
Matches 31; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 123 GGACGAGCCAGAGAGCGGGCTTGAGAGTACGCTGAGAGGGGG 169
Db 1 GGAGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGG 47

RESULT 52
AX162478 51 bp DNA linear PAT 22-JUN-2001
LOCUS AX162478
DEFINITION Sequence 5806 from Patent WO0140521.
ACCESSION AX162478
VERSION AX162478.1 GI:14543809
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
AUTHORS Shinkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 5806 07-JUN-2001;
Curagen Corporation (US)

FEATURES					
source	location/Qualifiers 1..51 /organism="Homo sapiens" /db_xref="taxon:9606"				
misc_feature					
26 /note="2 of 2 allelic variants (5805 is other entry) Accession number CG44035239"					
BASE COUNT	18 a 2 c 5 g 26 t				
ORIGIN					
Query Match 0.9%; Score 21.4; DB 6; Length 51; Best Local Similarity 66.0%; Pred. No. 2.4e+06; Matches 31; Conservative 0; Mismatches 16; Indels 0; Gaps 0;					
OY	2097 AACACCGAATCTTTTATTATAATAATATTTTCCAATACA 2143 Db 48 AACAAATATATATATCTCTATATATATATAGCTGATAA 2				
RESULT 53					
LOCUS	I29928 55 bp DNA linear PAT 06-FEB-1997				
DEFINITION	Sequence 41 from patent US 5578468.				
ACCESSION	I29928				
VERSION	I29928.1 GI:1820719				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified. 1 (bases 1 to 55) Pickup,D.J., Patel,P. and Antczak,J.B. Site-specific RNA cleavage Patent: US 5578468-A 41-26-NOV-1996; Location/Qualifiers 1..55 /organism="unknown"				
BASE COUNT	47 a 2 c 1 g 5 t				
ORIGIN					
Query Match 0.9%; Score 21.4; DB 6; Length 55; Best Local Similarity 66.0%; Pred. No. 2.4e+06; Matches 31; Conservative 0; Mismatches 16; Indels 0; Gaps 0;					
OY	1754 GATTTAAAAATCAATCATGTGCMAAAAAAAAAACTTAAGCMAA 1800 Db 8 GATTTATATAAAAAIAAAAAAAAAAAAAAAAAAAAAAAAAA 54				
RESULT 54					
LOCUS	I66359 60 bp DNA linear PAT 28-DEC-1997				
DEFINITION	Sequence 18 from patent US 5670330.				
ACCESSION	I66359				
VERSION	I66359.1 GI:2724336				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified. 1 (bases 1 to 60) Sorensberg,N., Katze,M.G., Roy,S., Koromilas,A.E. and Barber,G.H. Anti-tumor agent assay using PCR Patent: US 5670330-A 18-23-SEP-1997; Location/Qualifiers 1..60 /organism="unknown"				
BASE COUNT	26 a 6 c 10 g 18 t				
ORIGIN					
Query Match 0.9%; Score 21.4; DB 6; Length 60; Best Local Similarity 61.8%; Pred. No. 2.4e+06; Matches 34; Conservative 0; Mismatches 21; Indels 0; Gaps 0;					
OY	644 TGGGGCAATTACATCAAAGGGGATATCTTACAGAGACCTGAAGCCGGGAATAT 698				

Db	5	TGGATTATATCATTCACAAAAAATTAATTCATPAGGATCTTAAGCCAGTATAT	59
RESULT 55			
LOCUS	AX160974/c	50 bp	DNA
DEFINITION	Sequence 4302 from Patent WO0140521.	linear	PAT 22-JUN-2001
ACCESSION	AX160974		
VERSION	AX160974.1	GI:14542305	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 50)		
AUTHORS	Shinkets,R.A. and Leach,M.		
TITLE	Nucleic acids containing single nucleotide polymorphisms and		
	methods of use thereof		
JOURNAL	Patent: WO 0140521-A 4302 07-JUN-2001;		
	Curagen Corporation (US)		
FEATRES	Location/Qualifiers		
SOURCE	1..50		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
misc_feature	25..26		
	/note="Nucleotide deleted between bases 25 and 26		
	Accession number cg43944408"		
misc_feature	26		
	/note="2 of 2 allelic variants (4301 is other entry)"		
BASE COUNT	12 a 13 c 7 g 18 t		
ORIGIN			
Query Match	0.9%; Score 21.2; DB 6; Length 50;		
Best Local Similarity	69.0%; Pred. No. 2.6e+06;		
Matches	29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;		
Db	895 GCACCCCATTCACCTGGGGAGATPAGAAAGAAACAATTGAC 936		
	46 GCATACCAATTTACTGGGGGAAAAAAGTTAGAGATGCC 5		
RESULT 56			
LOCUS	AX157225/c	51 bp	DNA
DEFINITION	Sequence 553 from Patent WO0140521.	linear	PAT 22-JUN-2001
ACCESSION	AX157225		
VERSION	AX157225.1	GI:14538556	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 51)		
AUTHORS	Shinkets,R.A. and Leach,M.		
TITLE	Nucleic acids containing single nucleotide polymorphisms and		
	methods of use thereof		
JOURNAL	Patent: WO 0140521-A 553 07-JUN-2001;		
	Curagen Corporation (US)		
FEATRES	Location/Qualifiers		
SOURCE	1..51		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
misc_feature	26		
	/note="1 of 2 allelic variants (554 is other entry)"		
	Accession number cg44938869"		
BASE COUNT	25 a 2 c 9 g 15 t		
ORIGIN			
Query Match	0.9%; Score 21.2; DB 6; Length 51;		
Best Local Similarity	64.0%; Pred. No. 2.6e+06;		
Matches	32; Conservative 0; Mismatches 18; Indels 0; Gaps 0;		

QY 2096 AACAACCTGAATCTTTTATATATATATATATTTTCAATGAT 2145
Db 51 AACAACCTGAATCTTTTATATATATATATATTTTATACCAAT 2

RESULT 57
AX160455/c 51 bp DNA linear PAT 22-JUN-2001
LOCUS AX160455
DEFINITION Sequence 3783 from Patent WO0140521.
ACCESSION AX160455
VERSION AX160455.1 GI:14541786
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 3783 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source location/Qualifiers
misc_feature 26
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="1 of 2 allelic variants (3784 is other entry)"
Accession number CG43920465"
BASE COUNT 24 a 6 c 8 g 13 t
ORIGIN

Query Match 0.9%; Score 21.2; DB 6; Length 51;
Best Local Similarity 64.0%; Pred.No.2.6e+06;
Matches 32; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 2102 CCTGAATCTTTTATATATATATATATTTTCAATGAT 2151
Db 51 CTTTATGTTCTAATATATCCAGATGACCTTGTAAATAGCTTTAT 2

RESULT 58
AR192747 54 bp DNA linear PAT 20-APR-2002
LOCUS AR192747
DEFINITION Sequence 8235 from patent US 6346398.
ACCESSION AR192747
VERSION AR192747.1 GI:20238712
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 54)
AUTHORS Pavco,P., McSwiggan,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 8235 12-FEB-2002;
FEATURES
source location/Qualifiers
BASE COUNT 21 a 9 c 14 g 10 t
ORIGIN

Query Match 0.9%; Score 21.2; DB 6; Length 54;
Best Local Similarity 64.0%; Pred.No.2.7e+06;
Matches 32; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 2045 AAAATGGAGGCAAGCAAAAGAACTTACATTTGATGTTTACGTG 2094
Db 2 AATGTGAGAGCAAGCAAGCAAGCAACCTTGTGTGATTTACCTG 51

RESULT 59
AF254565/c

LOCUS AF254565 54 bp DNA linear PRI 30-OCT-2000
DEFINITION Homo sapiens ATP7B (ATP7B) gene, exon 8 and partial cds.
ACCESSION AF254565
VERSION AF254565.1 GI:11037272
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 54)
AUTHORS Wang,N., Wu Z.Y., MuRong,S.X., Lin,M.T. and Fang,L.
TITLE Hot point mutations of Wilson disease gene in Chinese with DNA sequencing
JOURNAL Chung-Hua Shen Ching Ko Tsa Chih 31, 20-23 (1998)
REFERENCE 2 (bases 1 to 54)
AUTHORS Wu,Z.Y., Wang,N. and MuRong,S.X.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) Department of Neurology, First Affiliated Hospital of Fujian Medical University, Chazhong Road 20, Fuzhou, Fujian 350005, P.R. China
FEATURES
source location/Qualifiers
1..54
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="13"
/map="13q14.3"
<1..>54
/gene="ATP7B"
<1..>54
/gene="ATP7B"
/product="ATP7B"
<1..>54
/gene="ATP7B"
/codon_start=1
/product="ATP7B"
/protein_id="AA027542.1"
/db_xref="GI:11037273"
/translation="DTEPMLFVFIALGIMLEH"
<1..>54
/gene="ATP7B"
/number=8
variation 41
/gene="ATP7B"
/note="compared to sequence with GenBank Accession Number U11300"
/replace="g"
BASE COUNT 7 a 18 c 15 g 14 t
ORIGIN

Query Match 0.9%; Score 21.2; DB 9; Length 54;
Best Local Similarity 64.0%; Pred.No.2.7e+06;
Matches 32; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 122 TGGACGACGACAGAGCGGGCTCTGAGATGACGTGAGAGGGGGGT 171
Db 53 TGTTCAGCCACAGACGCCAGGCGCATGAACACAAACAGCATGGGGGGGT 4

RESULT 60
A43625/c 55 bp DNA linear PAT 06-MAR-1997
LOCUS A43625
DEFINITION Sequence 15 from Patent WO9507987.
ACCESSION A43625
VERSION A43625.1 GI:2298827
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 55)
AUTHORS Bublort,M., de,W.C., Coliau,D. and Roux-Salengien,P.
TITLE NOVEL PROTEINS/POLYPEPTIDES AND COTRANSFECTION PLASMIDS AND LIVE RECOMBINANT CARRIERS THEREFOR
JOURNAL Patent: WO 9507987-A 15 23-MAR-1995;

COMMENT SOLVAY (BE)
Other publication NO 961086 960509
Other publication ZA 9406887 950627
Other publication AU 7615894 950403
Other publication GB 2282601 950412.

FEATURES
source
1. .56
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 19 a 10 c 8 g 18 t
ORIGIN

Query Match 0.9%; Score 21.2; DB 6; Length 55;
Best Local Similarity 64.0%; Pred. No. 2.7e+06;
Matches 32; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1273 CCATCTGTAAGTGAAGTGAAGAAAGTTTCCTTGAACCAAAAT 1322
DB 50 CAAAATGACTCATGTGGGATCCTTTGTTAGTTCAACCAAAAT 1

RESULT 61
LOCUS A80902 56 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 13 from Patent EP0919631.
ACCESSION A80902
VERSION A80902.1 GI:6731507
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 56)
AUTHORS Goetz,F.P. and Pohlner,J.D.
TITLE Process for the identification of nucleic acids
JOURNAL Patent: EP 0919631-A 13 02-JUN-1999;
EVOTEC BIOSYSTEMS AG (DE)
LOCATION/Qualifiers

FEATURES
source
1. .56
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 23 a 11 c 12 g 10 t
ORIGIN

Query Match 0.9%; Score 21.2; DB 6; Length 56;
Best Local Similarity 69.0%; Pred. No. 2.7e+06;
Matches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 221 GCATGGAACATTGTGGAATTTGAAATCTCAGAACTAGTG 262
DB 9 GCTTACCACAACTTAAGAAATCTGAATATCTCAGCAAGTG 50

RESULT 62
LOCUS A97341 56 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 13 from Patent WO9916900.
ACCESSION A97341
VERSION A97341.1 GI:6780700
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 56)
AUTHORS Goetz,F. and Straus,A.
TITLE METHOD FOR IDENTIFYING A NUCLEIC ACID
JOURNAL Patent: WO 9916900-A 13 08-APR-1999;
GOETZ FRIEDRICH (DE); STRAUS ANDREAS (DE)
LOCATION/Qualifiers

FEATURES
source
1. .56
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 23 a 11 c 12 g 10 t
ORIGIN

Query Match 0.9%; Score 21.2; DB 6; Length 56;
Best Local Similarity 69.0%; Pred. No. 2.7e+06;
Matches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 221 GCATGGAACATTGTGGAATTTGAAATCTCAGAACTAGTG 262
DB 9 GCTTACCACAACTTAAGAAATCTGAATATCTCAGCAAGTG 50

RESULT 63
LOCUS A97358 56 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 13 from Patent WO9916904.
ACCESSION A97358
VERSION A97358.1 GI:6780716
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 56)
AUTHORS Goetz,F. and Straus,A.
TITLE METHOD FOR DETERMINING ACTIVE AGENTS
JOURNAL Patent: WO 9916904-A 13 08-APR-1999;
GOETZ FRIEDRICH (DE); STRAUS ANDREAS (DE)
LOCATION/Qualifiers

FEATURES
source
1. .56
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 23 a 11 c 12 g 10 t
ORIGIN

Query Match 0.9%; Score 21.2; DB 6; Length 56;
Best Local Similarity 69.0%; Pred. No. 2.7e+06;
Matches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 221 GCATGGAACATTGTGGAATTTGAAATCTCAGAACTAGTG 262
DB 9 GCTTACCACAACTTAAGAAATCTGAATATCTCAGCAAGTG 50

RESULT 64
LOCUS A97358 56 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 13 from patent US 6339174.
ACCESSION A97358
VERSION A97358.1 GI:2026278
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 56)
AUTHORS Bogdanovic,S.
TITLE Method for preparing aldehydes by hydroformylation
JOURNAL Patent: US 6339174-A 13 15-JAN-2002;
LOCATION/Qualifiers

FEATURES
source
1. .56
/organism="unknown"

BASE COUNT 23 a 11 c 12 g 10 t
ORIGIN

Query Match 0.9%; Score 21.2; DB 6; Length 56;
Best Local Similarity 69.0%; Pred. No. 2.7e+06;
Matches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 221 GCATGGAACATTGTGGAATTTGAAATCTCAGAACTAGTG 262
DB 9 GCTTACCACAACTTAAGAAATCTGAATATCTCAGCAAGTG 50

RESULT 65
LOCUS E07494 38 bp DNA linear PAT 29-SEP-1997


```

DEFINITION Synthetic DNA for probe.
ACCESSION E07494
VERSION E07494.1 GI:2175632
KEYWORDS JP 1994133799-A/3.
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE
  1 (bases 1 to 38)
  Yamamoto, K., Yamamoto, T. and Mori, H.
  ANALYSIS OF HUMAN HERPES VIRUS 6 TYPE @ (3754/24) HHV-6) DNA AND
  DISCRIMINATION OF SUB-TYPE
  Patent: JP 1994133799-A 3 17-MAY-1994;
  INTERNATL REAGENTS CORP

COMMENT
  OS None
  OC Artificial sequences.
  PN JP 1994133799-A/3
  PD 17-MAY-1994
  PF 27-OCT-1992 JP 1992311416
  PI YAMAMOTO KOICHI, YAMAMOTO TAKESHI, MORI HIROYUKI PC
  CI Q1/68, C12Q1/68, C12N15/11, C12N15/38;
  CC strandedness: single;
  CC topology: linear;
  CC hypothetical: No;
  CC anti-sense: No;
  FH Key
  FH Location/Qualifiers
  FT source
  FT 1.38
  FT /organism='Artificial sequences'.
  FT 1.38
  FT /db_xref='taxon:32644'

FEATURES
  source
  BASE COUNT 16 a 5 c 5 g 12 t
  ORIGIN
  Query Match 0.9%; Score 21; DB 6; Length 38;
  Best Local Similarity 73.0%; Pred. No. 2.9e+06;
  Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1749 ACGTGATTTTAAATAATCAATCAATGTCGCAAAAA 1785
Db 1 ATGTGAATGTAAATAATTAATTAATCGCCGCAAAAA 37

RESULT 66
LOCUS AX299737 40 bp DNA linear PAT 26-NOV-2001
DEFINITION Sequence 17 from Patent WO0175163.
ACCESSION AX299737
VERSION AX299737.1 GI:17129277
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Landers, J. B.
TITLE High throughput methods for haplotyping
JOURNAL Patent: WO 0175163-A 17 11-OCT-2001;
POLYMERX, Inc. (US)
FEATURES
  source
  1.40
  /organism='synthetic construct'
  /db_xref='taxon:32630'
  /note='Synthetic Oligonucleotide'

misc feature
  1 /note='amino group attached'
  7 a 4 c 3 g 26 t

BASE COUNT 7 a 4 c 3 g 26 t
ORIGIN
  Query Match 0.9%; Score 21; DB 6; Length 40;
  Best Local Similarity 73.0%; Pred. No. 2.9e+06;
  Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy 1766 TCATCAATGTCGCAAAAAAACTTAAGCAATA 1802
Db 37 TCATTCATTGTGGCAAAAAAACTTAAGCAATA 1

RESULT 67
LOCUS AX160105 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 3433 from Patent WO0140521.
ACCESSION AX160105
VERSION AX160105.1 GI:14541436
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
  1 (bases 1 to 51)
  Shimkets, R.A. and Beach, M.
  Nucleic acids containing single nucleotide polymorphisms and
  methods of use thereof
  Patent: WO 0140521-A 3433 07-JUN-2001;
  Curagen Corporation (US)
FEATURES
  source
  1.51
  /organism='Homo sapiens'
  /db_xref='taxon:9606'

misc feature
  26 /note='1 of 2 allelic variants (3434 is other entry)'
  26 /accession number Cg4326348'

BASE COUNT 25 a 6 c 6 g 14 t
ORIGIN
  Query Match 0.9%; Score 21; DB 6; Length 51;
  Best Local Similarity 66.7%; Pred. No. 2.9e+06;
  Matches 30; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1733 GACACGAGAAAAATACGTCGATTTTAAAAATCAATCAATGCT 1777
Db 6 GAACAGATTAATAAAAAATAGTTGAACACATATATCTTCGT 50

RESULT 68
LOCUS MUSBMP24H 56 bp DNA linear ROD 29-MAY-2002
DEFINITION Mouse gene for BMP-2/4 type I receptor, exons (partial) and introns
(partial).
ACCESSION D45009
VERSION D45009.1 GI:624892
KEYWORDS BMP-2/4 type I receptor.
SOURCE Mus musculus (sub species: domesticus, strain:129) adult male liver
DNA, clone lib: lambda DASH-II.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 56)
  Mishina, Y., Suzuki, A., Debra, G.J., Copeland, N.G., Jenkins, N.A.,
  Ueno, N. and Behringer, R.R.
  Genomic organization and chromosomal location of the mouse type I
  BMP-2/4 receptor
  Biochem. Biophys. Res. Commun. (1995) In press
  Behringer, R.R.
  Direct Submision
  Submitted (30-DEC-1994) Richard R. Behringer, The University of
  Texas M.D. Anderson Cancer Center, Molecular Genetics, 1515
  Holcombe, Houston, Texas 77030, U.S.A.
  (E-mail:rs11112@odn.mda.utx.tmc.edu, Tel:713-794-4631,
  Fax:713-794-4394)
FEATURES
  source
  1.56
  /organism='Mus musculus'
  /strain='129'
  /sub_species='domesticus'

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	/db_xref="taxon:10090"
	/chromosome="14"
exon	/sex="male"
	/issue_type="liver"
	/clone_id="lambda DASH-II"
	/dev_stage="adult"
	<1..10
	/product="BMP-2/4 type I receptor"
	/note="the length of exons is 100 bp"
intron	/number=5
	11..>56
	/note="the lengtgh of introns is 4.8 kb"
BASE COUNT	19 a 5 c 4 g 28 t
ORIGIN	
Query Match	0.9%; Score 21; DB 10; Length 56;
Best Local Similarity	73.0%; Pred. No. 3e+06;
Matches	27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
OY	2093 TGCAACAACTGATCTTTTATTATAAATAT 2129 Dn 3 TGTATAGTAGACTTATTATTACAATATAT 39
RESULT 69	
LOCUS	AR209950 59 bp DNA linear PAT 20-JUN-2002
DEFINITION	Sequence 4 from patent US 6387631.
ACCESION	AR209950
VERSION	AR209950.1 GI:21512053
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 59)
AUTHORS	Arnold,L.J., Sawan,S.P. and Lee,P.H.
TITLE	Polymer coated surfaces for microarray applications
JOURNAL	Patent: US 6387631-A 4 14-MAY-2002;
FEATURES	. Location/Qualifiers
source	1..59
	/organism="unknown"
BASE COUNT	25 a 4 c 12 g 18 t
ORIGIN	
Query Match	0.9%; Score 21; DB 6; Length 59;
Best Local Similarity	66.7%; Pred. No. 3e+06;
Matches	30; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
OY	1078 TTCTTTAGACATTTA CTGGGAAGA ACTTCGTGC TCGAAAAGTG 1122 Db 5 TTCATTAGTGACATT TAAGA GA AACTG ATGTTTGA AAATGTG 49
RESULT 70	
LOCUS	AX253387 59 bp DNA linear PAT 10-OCT-2001
DEFINITION	Sequence 17 from Patent WO0171039.
ACCESION	AX253387
VERSION	AX253387.1 GI:16073921
KEYWORDS	.
SOURCE	Candida albicans.
ORGANISM	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyces;
REFERENCE	1 (bases 1 to 59)
AUTHORS	Reynolds,M.A., Ruvoio,M. and Arnold,L.J.
TITLE	Combined polynucleotide sequences as discrete assay endpoints
JOURNAL	Patent: WO 0171039-A 17 27-SEP-2001;
FEATURES	Incyte Pharmaceuticals, Inc. (US) . Location/Qualifiers
source	1..59
	/organism="Candida albicans"
BASE COUNT	12 a 16 c 13 g 13 t 6 others
ORIGIN	
Query Match	0.9%; Score 21; DB 6; Length 60;
Best Local Similarity	62.8%; Pred. No. 3e+06;
Matches	27; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
OY	58 TACCCAGCCCCGACCTTCGAGACAGGGAAGCTGAGCATGTG 100
	/db_xref="taxon:5476"
	/note="Incyte ID No: F23805"
BASE COUNT	25 a 4 c 12 g 18 t
ORIGIN	
Query Match	0.9%; Score 21; DB 6; Length 59;
Best Local Similarity	66.7%; Pred. No. 3e+06;
Matches	30; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
OY	1078 TTCTTTAGACATTTA CTGGGAAGA ACTTCGTGC TCGAAAAGTG 1122 Db 5 TTCATTAGTGACATT TAAGA GA AACTG ATGTTTGA AAATGTG 49
RESULT 72	
LOCUS	AR073297 60 bp DNA linear PAT 28-AUG-2000
DEFINITION	Sequence 2 from patent US 5948694.
ACCESION	AR073297
VERSION	AR073297.1 GI:10000060
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 60)
AUTHORS	Berry,M.J., Davis,P.J., Verhoeven,M.E. and De Winter,R.F.J.
TITLE	Immunoadorbent reagents
JOURNAL	Patent: US 5948694-A 2 07-SEP-1999;
FEATURES	. Location/Qualifiers
source	1..60
	/organism="unknown"
BASE COUNT	12 a 16 c 13 g 13 t 6 others
ORIGIN	
Query Match	0.9%; Score 21; DB 6; Length 60;
Best Local Similarity	62.8%; Pred. No. 3e+06;
Matches	27; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
OY	58 TACCCAGCCCCGACCTTCGAGACAGGGAAGCTGAGCATGTG 100

Db 17 TACCCCTTACCGAATCCCNNNNGATCCTGAGAGACG 59

RESULT 73
LOCUS YSCMTp191/c 60 bp DNA linear PLN 04-AUG-1993
DEFINITION Yeast (S.cerevisiae) mitochondrial petite mutant excision seq 19,
left end.
ACCESSION J01506.1 GI:343885
VERSION J01506.1
KEYWORDS AT-rich region; GC rich region.
SEGMENT 1 of 2
SOURCE Yeast (Saccharomyces cerevisiae) mitochondrial DNA.
ORGANISM Mitochondrion Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
REFERENCE 1 (bases 1 to 60)
AUTHORS de Zamaroczy,M., Faugeron-Fonty,G. and Bernardi,G.
TITLE Excision sequences in the mitochondrial genome of yeast
JOURNAL Gene 21 (3), 193-202 (1983)
MEDLINE 83210931
PubMed 6343188

COMMENT Additional sequences reported in [1], but sequenced in earlier
papers, appear in separate entries. Excision repeat corresponds to
bases 11 to 36.
Location/Qualifiers
1..60
/organism="Saccharomyces cerevisiae"
/db_xref="taxon:4932"

BASE COUNT 32 a 2 c 0 g 26 t
ORIGIN

Query Match 0.9%; Score 21; DB 8; Length 60;
Best Local Similarity 82.8%; Pred. No. 3e+06; 5; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2111 TTTTATATATAATATATATATTTTCAAA 2139
Db 37 TATTATATATATATATATATTTTATTA 9

RESULT 74
LOCUS AF177252 57 bp RNA linear INV 21-FEB-2000
DEFINITION Bodo saltans clone pBG764 mitochondrial putative gRNA.
ACCESSION AF177252
VERSION AF177252.1 GI:7012655
KEYWORDS
SOURCE Bodo saltans.
ORGANISM Mitochondrion Bodo saltans
Eukaryota; Euglenozoa; Kinetoplastida; Bodonidae; Bodo.
REFERENCE 1 (bases 1 to 57)
AUTHORS Blom,D., de Haan,A., van den Burg,J., van den Berg,M., Sloof,P.,
Jirku,M., Lukes,J. and Benne,R.
TITLE Mitochondrial multicircles in the free-living bodonid Bodo saltans
contain two gRNA gene cassettes and are not found in large networks
JOURNAL RNA 6 (1), 121-135 (2000)
MEDLINE 20132239
PubMed 10668805

REFERENCE 2 (bases 1 to 57)
AUTHORS Blom,D., De Haan,A., Sloof,P., Jirku,M., Lukes,J. and Benne,R.
TITLE Direct Submission
JOURNAL Submitted (12-AUG-1999) Department of Biochemistry, Academic
Medical Center, Meibergdreef 15, Amsterdam 1105 AZ, The Netherlands
Location/Qualifiers
1..57
/organism="Bodo saltans"
/db_xref="taxon:75058"
/chromosome="multicircle"
/clone="pBG764"
1..57

misc_RNA

BASE COUNT 23 a 10 c 4 g 20 t
ORIGIN

Query Match 0.9%; Score 20.8; DB 3; Length 57;
Best Local Similarity 60.7%; Pred. No. 3.3e+06; 22; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 2062 ACAAGAAGAACTTACCATGATGTTTACGTCGAACACCTGAATCTTTT 2117
Db 2 ACAAAACACACACAGCATTAAGCTATCAACGAACATTTT 57

RESULT 75
LOCUS A48423 28 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 46 from Patent WO9603501.
ACCESSION A48423
VERSION A48423.1 GI:2302214
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Chaudhuri,B., Stephan,C. and Fuerst,P.
TITLE DUAL HYBRID SYSTEM
JOURNAL Patent: WO 9603501-A 46 08-FEB-1996;
CIBA GEIGY AG (CH)
COMMENT Other publication AU 2983295 960222.
Location/Qualifiers
1..28
/organism="unidentified"
/db_xref="taxon:32644"
/note="5'END ANTI-SENSE STRAND OF CODING SEQUENCE OF RAT
P7056 KINASE GENE"
/function="PCR FRAGMENT"

BASE COUNT 11 a 5 c 6 g 6 t
ORIGIN

Query Match 0.9%; Score 20.6; DB 6; Length 28;
Best Local Similarity 85.2%; Pred. No. 3.5e+06; 4; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1376 AATTTTCCTCGGGAGTTCTGGGAA 1402
Db 28 AATTCCTCGGGAGTTCTGTAGAA 2

RESULT 76
LOCUS A48424 28 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 47 from Patent WO9603501.
ACCESSION A48424
VERSION A48424.1 GI:2302215
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Chaudhuri,B., Stephan,C. and Fuerst,P.
TITLE DUAL HYBRID SYSTEM
JOURNAL Patent: WO 9603501-A 47 08-FEB-1996;
CIBA GEIGY AG (CH)
COMMENT Other publication AU 2983295 960222.
Location/Qualifiers
1..28
/organism="unidentified"
/db_xref="taxon:32644"
/complement(9..28)
/note="5'END ANTI-SENSE STRAND OF CODING SEQUENCE OF
TRUNCATED P7056K DELTA C GENE"

misc_peptide

BASE COUNT 9 a /function="PCR FRAGMENT"
ORIGIN 5 c 5 g 9 t

Query Match 0.9%; Score 20.6; DB 6; Length 28;
Best Local Similarity 85.2%; Pred. No. 3.5e+06;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1586 ACCTGGTATGATCATGACAGCA 1612
DB 28 ACCTGGTATGATCATGATCA 2

RESULT 77
LOCUS A51711 50 bp DNA linear PAT 10-MAR-1997
DEFINITION Sequence 17 from Patent WO9618744.
ACCESSION A51711
VERSION A51711.1 GI:2304515
KEYWORDS

SOURCE unidentified.
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 50)
AUTHORS Crozet,J., Scherman,D. and Wils,P.
TITLE PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN IMMOBILIZED OLIGONUCLEOTIDE
JOURNAL Patent: WO 9618744-A 17 20-JUN-1996;
Rhone Poulenc Korer SA (FR)
OTHER PUBLICATION AU 4178996 960703
Other publication FR 2728264 960621.
FEATURES Location/Qualifiers

source 1..50
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 17 a 0 c 33 g 0 t
ORIGIN

Query Match 0.9%; Score 20.6; DB 6; Length 50;
Best Local Similarity 67.4%; Pred. No. 3.6e+06;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 132 AGAGGACGGCGCTGTGAGATGAGCTGGAGGCGGTCTAG 174
DB 3 AGAGGACGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 45

RESULT 78
LOCUS ARI67590 50 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 17 from patent US 6287762.
ACCESSION ARI67590
VERSION ARI67590.1 GI:17903379
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 50)
AUTHORS Crozet,J., Scherman,D. and Wils,P.
TITLE Purification of a triple helix formation with an immobilized oligonucleotide
JOURNAL Patent: US 6287762-A 17 11-SEP-2001;
FEATURES Location/Qualifiers

source 1..50
/organism="unknown"
BASE COUNT 17 a 0 c 33 g 0 t
ORIGIN

Query Match 0.9%; Score 20.6; DB 6; Length 50;
Best Local Similarity 67.4%; Pred. No. 3.6e+06;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 132 AGAGGACGGCGCTGTGAGATGAGCTGGAGGCGGTCTAG 174

DB 3 AGAGGACGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 45

RESULT 79
LOCUS ARI78300 50 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 17 from patent US 6319672.
ACCESSION ARI78300
VERSION ARI78300.1 GI:20219438
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 50)
AUTHORS Crozet,J., Scherman,D., Wils,P., Blanche,F. and Cameron,B.
TITLE Purification of a triple helix formation with an immobilized oligonucleotide
JOURNAL Patent: US 6319672-A 17 20-NOV-2001;
FEATURES Location/Qualifiers

source 1..50
/organism="unknown"
BASE COUNT 17 a 0 c 33 g 0 t
ORIGIN

Query Match 0.9%; Score 20.6; DB 6; Length 50;
Best Local Similarity 67.4%; Pred. No. 3.6e+06;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 132 AAGAGACGGCGCTGTGAGATGAGCTGGAGGCGGTCTAG 174
DB 3 AAG 45

RESULT 80
LOCUS AXI65034 50 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 229 from Patent WO0138586.
ACCESSION AXI65034
VERSION AXI65034.1 GI:14545863
KEYWORDS

SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 50)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
Shinkens,R.A. and Leach,M.
Nucleic acids containing single nucleotide polymorphisms and
method of use thereof
Patent: WO 0138586-A 229 31-MAY-2001;
JOURNAL Curagen Corporation (US)
FEATURES Location/Qualifiers

source 1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"

misc_feature 25..26
/note="Nucleotide deleted between bases 25 and 26
Accession number cg42907867"

variation 26
/note="single nucleotide polymorphism"
BASE COUNT 9 a 8 c 21 g 12 t
ORIGIN

Query Match 0.9%; Score 20.6; DB 6; Length 50;
Best Local Similarity 74.3%; Pred. No. 3.6e+06;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2301 TGGGGTGACCTGGGGTTATTTGAGTAACCCAG 2335
DB 15 TGGAGGAGATCTGGCGTTTCTGAAGCCAG 49

RESULT 81

AX323382
LOCUS AX323382 50 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 17 from Patent WO0192511.
ACCESSION AX323382
VERSION AX323382.1 GI:18094144
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Crouzet, J., Scherman, D., Wils, P., Blanche, F. and Cameron, B.
TITLE Publication of a triple helix formation with an immobilized oligonucleotide
JOURNAL Patent: WO 0192511-A 17 06-DEC-2001;
Aventis Pharma (PR)
FEATURES
SOURCE location/Qualifiers
1..50
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

BASE COUNT 17 a 0 c 33 g 0 t
ORIGIN
Query Match 0.9%; Score 20.6; DB 6; Length 50;
Best Local Similarity 67.4%; Pred. No. 3.6e+06;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 132 AAGAGACGGGGCTCTGAGATGAGTGGAGGCGGGTCA 174
Db 3 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 45

RESULT 82
LOCUS AR068824 51 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 24 from patent US 5854051.
ACCESSION AR068824
VERSION AR068824.1 GI:6001031
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 51)
AUTHORS Chandrasekar, R. and Tsuji, N.
TITLE Parasitic helminth asparaginase proteins, nucleic acid molecules, and uses thereof
JOURNAL Patent: US 5854051-A 24 29-DEC-1998;
FEATURES
SOURCE location/Qualifiers
1..51
/organism="unknown"

BASE COUNT 12 a 12 c 5 g 22 t
ORIGIN
Query Match 0.9%; Score 20.6; DB 6; Length 51;
Best Local Similarity 67.4%; Pred. No. 3.6e+06;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1848 CATCTTCTCAACCTTATCAGAGATTTCATGTTGATGACTCG 1890
Db 9 CTTCTTACTGAACTTTTTCATCTTTTCTTCTATGACTAG 51

RESULT 83
LOCUS AR122557 51 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 24 from patent US 6165735.
ACCESSION AR122557
VERSION AR122557.1 GI:14106874
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 51)

AUTHORS Chandrasekar, R. and Tsuji, N.
TITLE Parasitic helminth asparaginase proteins, nucleic acid molecules, and uses thereof
JOURNAL Patent: US 6165735-A 24 26-DEC-2000;
FEATURES
SOURCE location/Qualifiers
1..51
/organism="unknown"

BASE COUNT 12 a 12 c 5 g 22 t
ORIGIN
Query Match 0.9%; Score 20.6; DB 6; Length 51;
Best Local Similarity 67.4%; Pred. No. 3.6e+06;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1848 CATCTTCTCAACCTTATCAGAGATTTCATGTTGATGACTCG 1890
Db 9 CTTCTTACTGAACTTTTTCATCTTTTCTTCTATGACTAG 51

RESULT 84
LOCUS AX157089 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 417 from Patent WO0140521.
ACCESSION AX157089
VERSION AX157089.1 GI:14538420
KEYWORDS
SOURCE human.
ORGANISM human.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 417 07-JUN-2001;
Curagen Corporation (US)
FEATURES
SOURCE location/Qualifiers
1..51
/organism="Homo sapiens"
/db_xref="taxon:9606"

misc-feature
/note="1 of 2 allelic variants (418 is other entry)
Accession number CG44924574"

BASE COUNT 15 a 15 c 14 g 7 t
ORIGIN
Query Match 0.9%; Score 20.6; DB 6; Length 51;
Best Local Similarity 67.4%; Pred. No. 3.6e+06;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1024 GCTTCTCGTCTGGAGAGCTGCTCGGAGAGCTGGAGAGATTC 1066
Db 48 GCTTCTCTCTGAGAGCTCTCGAGCTGGGAGCTGATCGATTC 6

RESULT 85
LOCUS AX157090 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 418 from Patent WO0140521.
ACCESSION AX157090
VERSION AX157090.1 GI:14538421
KEYWORDS
SOURCE human.
ORGANISM human.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 418 07-JUN-2001;
Curagen Corporation (US)
FEATURES
SOURCE location/Qualifiers

source 1. .51
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc_feature 26
/note="2 of 2 allelic variants (417 is other entry)
Accession number CG44924574"
BASE COUNT 15 a 14 c 14 g 8 t
ORIGIN

Query Match 0.9%; Score 20.6; DB 6; Length 51;
Best Local Similarity 67.4%; Pred. No. 3.6e+06;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1024 GCTTCTGCTGGAGAGCTGCTCCGAGCGCTGAGAGATTTC 1066
Db 48 GCTTCTGCTGGAGAGCTGCTCCGAGCGCTGAGATCAGTTTC 6

RESULT 86
AX158178 AX158178 51 bp DNA linear PAT 22-JUN-2001
LOCUS AX158178
DEFINITION Sequence 1506 from Patent WO0140521.
ACCESSION AX158178
VERSION AX158178.1 GI:14539509
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 1506 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
misc_feature 1. .51
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="2 of 2 allelic variants (1505 is other entry)
Accession number CG30144940"
BASE COUNT 15 a 19 c 9 g 8 t
ORIGIN

Query Match 0.9%; Score 20.6; DB 6; Length 51;
Best Local Similarity 62.7%; Pred. No. 3.6e+06;
Matches 32; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 669 CATCTACAGAGCCTGAGCGGAGATATCATGCTTAATCACCAGGTCA 719
Db 1 CATCTACGAGAGCTGAGCGGAGATATCTTGTCAACACCCGGGAGCA 51

RESULT 87
AX161887/c AX161887 51 bp DNA linear PAT 22-JUN-2001
LOCUS AX161887
DEFINITION Sequence 5215 from Patent WO0140521.
ACCESSION AX161887
VERSION AX161887.1 GI:14543218
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 5215 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1. .51

misc_feature 26
/note="1 of 2 allelic variants (5216 is other entry)
Accession number CG43986974"
BASE COUNT 12 a 10 c 14 g 15 t
ORIGIN

Query Match 0.9%; Score 20.6; DB 6; Length 51;
Best Local Similarity 67.4%; Pred. No. 3.6e+06;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1145 TGCATCTGAGAGAGATGTAAGTCAAGTTGATTCAGATTAC 1187
Db 46 TGCAGAGTCAGAGGAGATTCCGACAGCTTCATCCCAATTCAC 4

RESULT 88
AX161888 AX161888 51 bp DNA linear PAT 22-JUN-2001
LOCUS AX161888
DEFINITION Sequence 5216 from Patent WO0140521.
ACCESSION AX161888
VERSION AX161888.1 GI:14543219
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 5216 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
misc_feature 1. .51
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="2 of 2 allelic variants (5215 is other entry)
Accession number CG43986974"
BASE COUNT 13 a 10 c 13 g 15 t
ORIGIN

Query Match 0.9%; Score 20.6; DB 6; Length 51;
Best Local Similarity 67.4%; Pred. No. 3.6e+06;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1145 TGCATCTGAGAGAGATGTAAGTCAAGTTGATTCAGATTAC 1187
Db 46 TGCAGAGTCAGAGGAGATTCCGACAGCTTCATCCCAATTCAC 4

RESULT 89
AX162091/c AX162091 51 bp DNA linear PAT 22-JUN-2001
LOCUS AX162091
DEFINITION Sequence 5419 from Patent WO0140521.
ACCESSION AX162091
VERSION AX162091.1 GI:14543422
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 5419 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1. .51
/organism="Homo sapiens"

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misc_feature          /db_xref="taxon:9606"
                      26
                      /note="1 of 2 allelic variants (5420 is other entry)
                      Accession number CG43999946"
BASE COUNT           25 a          7 c          6 g          13 t
ORIGIN

Query Match          0.9%; Score 20.6; DB 6; Length 51;
Beat Local Similarity 74.3%; Pred. No. 3.6e+06;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Cy 2098 ACAACCTGAATCTTTTATATATATATATATTT 2132
      ||||| | | | | | | | | | | | | | | | |
Db 49 ACAACAGGTATGTTTGTTCAGAAATATGTAATT 15

RESULT 91
AX404671/c           53 bp      DNA      linear      PAT 14-JUN-2002
LOCUS                AX404671
DEFINITION           Sequence 45 from Patent WO0224745.
ACCESSION            AX404671
VERSION              AX404671.1 GI:21437952
KEYWORDS
SOURCE               human.
ORGANISM             Homo sapiens
REFERENCE            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS             Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE               Abken, H. and Schinkoethe, T.
JOURNAL             Method for detecting tumor cells
                   Patent: WO 0224745-A 45 28-MAR-2002;
                   Abken, Hinrich (DE)
FEATURES             Location/Qualifiers
                     1..53
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT           22 a          6 c          6 g          19 t

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ORIGIN	Query Match	0.9%	Score 20.6	DB 6	Length 53
Query Match	Best Local Similarity	62.7%	Pred. No. 3.7e+06		
Matches	32	Conservative	0	Mismatches 19	Indels 0
Gaps	0				
Db	2109	CTTTTCTTATATAAATATATATATTTTCAADPAGTTTGTGACGCTCA	2159		
52	CTTTTCTTACTACTTTGAAAAAGTTGCTAATATGATATATGAAACATGCA	2			
RESULT 92	AF328254/c	54 bp	DNA	linear	ROD 29-JUN-2001
LOCUS	AF328254				
DEFINITION	Mus musculus isolate 1.2-N1 T-cell junctional region gene, partial cds.				
ACCESSION	AF328254				
VERSION	AF328254.1				
KEYWORDS	GI:13898468				
SOURCE	Mus musculus.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 54)				
TITLE	Maryanski, J.L., Atcuil, V., Hamrouni, A., Mutin, M., Rossi, M., Audlin, A. and Bucher, P.				
JOURNAL	Individuality of Ag-selected and preimmune TCR repertoires				
MEDLINE	Immunol. Res. 23 (1), 75-84 (2001)				
PUBMED	21310440				
REFERENCE	11417861				
AUTHORS	2 (bases 1 to 54)				
TITLE	Maryanski, J.L., Atcuil, V., Hamrouni, A., Mutin, M., Rossi, M., Audlin, A. and Bucher, P.				
JOURNAL	Direct Submission				
DEFINITION	Submitted (13-DEC-2000) INSERM Unit 503, CERVI, 21 Avenue Tony Garnier, 69365 Lyon Cedex 07, France				
FEATURES	Location/Qualifiers				
SOURCE	1..54				
	/organism="Mus musculus"				
	/strain="DBA/2"				
	/isolate="1.2-N1"				
	/db_xref="taxon:10090"				
	/rearranged				
	<1..>54				
	/product="T-cell receptor beta chain VDJ junctional region"				
	<1..>54				
	/note="TCRBV1.0"				
	/codon_start=1				
	/product="T-cell receptor beta chain VDJ junctional region"				
	/protein_id="AAK48763.1"				
	/db_xref="GI:13898468"				
	/translation="SAVYVLCASSIIONSDYTFG"				
BASE COUNT	11 a	18 c	10 g	15 t	
ORIGIN					
Query Match	0.9%	Score 20.6	DB 10	Length 54	
Best Local Similarity	67.4%	Pred. No. 3.7e+06			
Matches	29	Conservative	0	Mismatches 14	Indels 0
Gaps	0				
Db	1638	AAGGTGAGAGGAGAGATGTGTGACGATCTTGCAAGTGAACA	1680		
50	AAGGTGAGTGGAGAGTTTGTGAAGCTGCTGCACAGAGATAC	8			
RESULT 93	E10890	60 bp	DNA	linear	PAT 29-SEP-1997
LOCUS	E10890				
DEFINITION	PCR primer for gaining human cytochrome P450.				
ACCESSION	E10890				
VERSION	E10890.1				
KEYWORDS	GI:22027985				
	JP 1996056695-A/39.				

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SOURCE      unidentified.
ORGANISM    unidentified.
REFERENCE   1 (bases 1 to 60)
AUTHORS     Hayashi,K., Sakaki,T., Yabusaki,Y., Komai,K., Kaneko,H. and
            Nakatsuka,I.
TITLE       METHOD FOR EVALUATING SAFETY
JOURNAL     Patent: JP 1996056695-A 39 05-MAR-1996;
            SUMITOMO CHEM CO LTD
COMMENT     OS None
            OC Artificial sequences.
            PN JP 1996056695-A/39
            PD 05-MAR-1996
            PR 15-JUL-1994 JP 1994164184
            PR 20-JUL-1993 JP 93P 201120, 30-JUL-1993 JP 93P 208279, PR
            PR 17-JUN-1994 JP 94P 136053
            PI HAYASHI KOJI, SAKAKI TOSHIYUKI, YABUSAKI YOSHIYASU, PI KOMAI
            KOICHIRO,
            PI KANEKO HIDEO, NAKATSUKA IWAO
            PC C12Q1/02.C12M1/34.C12Q1/26;
            CC strandedness: Single;
            CC topology: Linear;
            CC hypothetical: No;
            FH Key
            FT source
            FT 1..60
            /organism='Artificial sequences'.
FEATURES
source      1..60
            Location/Qualifiers
            1..60
            /organism="unidentified"
            /db_xref="taxon:32644"
BASE COUNT 24 a 12 c 17 g 7 t
ORIGIN
Query Match 0.9%; Score 20.6; DB 6; Length 60;
Best Local Similarity 62.7%; Pred. No. 3.7e+06;
Matches 32; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 888 GACTGAGGACCCCATTCACCTGGGAGATAGAGAAAGAAACATTGACAA 938
DB 10 GAATGAGGACACCTGATAGAGGCGGAGACAGAGCAATTCATTGACAA 60

RESULT 94
LOCUS       AX117117 51 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 2240 from Patent WO0129262.
ACCESSION  AX117117
VERSION     AX117117.1 GI:14034059
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 51)
AUTHORS     Picoult-Newburg,L. and Pohl,M.
TITLE       Gentotyping reagents, kits and methods of use thereof
JOURNAL     Patent: WO 0129262-A 2240 26-APR-2001;
            Orchid Biosciences, Inc. (US)
FEATURES
source      1..51
            Location/Qualifiers
            1..51
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
BASE COUNT 25 a 7 c 7 g 11 t 1 others
ORIGIN
Query Match 0.9%; Score 20.4; DB 6; Length 51;
Best Local Similarity 65.2%; Pred. No. 4.1e+06;
Matches 30; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 1724 AACACTTCGACACAGGAAATATAACGTGATTTTAAAAATCAA 1769
DB 2 ACGAATTCAACAGAGGAGAAAAAACTATTAATTGCGAGAAATCTA 47

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RESULT 95
LOCUS       YSCMTPI82 57 bp DNA linear PLN 04-AUG-1993
DEFINITION Yeast (S.cerevisiae) mitochondrial petite mutant excision seq 18,
            right end.
ACCESSION  J01505.1 GI:343883
VERSION     J01505.1
KEYWORDS    AT-rich region; GC rich region.
SEGMENT     2 of 2
SOURCE      Yeast (Saccharomyces cerevisiae) mitochondrial DNA.
ORGANISM    Mitochondrion Saccharomyces cerevisiae
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE   1 (bases 1 to 57)
AUTHORS     de Zamaroczy,M., Faugeton-Fonty,G. and Bernardi,G.
TITLE       Excision sequences in the mitochondrial genome of yeast
JOURNAL     Gene 21 (3), 193-202 (1983)
MEDLINE     83210931
PUBMED      6343188
COMMENT     Additional sequences reported in [1], but sequenced in earlier
            papers, appear in separate entries. Excision repeat corresponds to
            bases 11 to 25.
FEATURES
source      1..57
            Location/Qualifiers
            1..57
            /organism="Saccharomyces cerevisiae"
            /organelle="mitochondrion"
            /db_xref="taxon:4932"
BASE COUNT 23 a 1 c 1 g 31 t 1 others
ORIGIN
Query Match 0.9%; Score 20.4; DB 8; Length 57;
Best Local Similarity 60.0%; Pred. No. 4.1e+06;
Matches 33; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 2118 ATATTAATATATATATTTTCAATAGATTGATTCAGCTCATTAAGAAAACAT 2172
DB 2 ATTAATATATTTATTTATTTAGTTTATTTTATTAACATTTTATTAATAAT 56

RESULT 96
LOCUS       A08918 39 bp DNA linear PAT 02-SEP-1993
DEFINITION H.sapiens (allele MS32, isolate English, serial number 3 and 4)
            minisatellite sequence.
ACCESSION  A08918
VERSION     A08918.1 GI:411840
KEYWORDS
SOURCE      Homo sapiens.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 39)
AUTHORS     Jeffreys,A.J.
TITLE       Extended nucleotide sequences
JOURNAL     Patent: EP 0370719-A 101 30-MAY-1990;
            IMPERIAL CHEMICAL INDUSTRIES PLC
FEATURES
source      1..39
            Location/Qualifiers
            1..39
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
BASE COUNT 18 a 0 c 0 g 21 t
ORIGIN
Query Match 0.9%; Score 20.2; DB 6; Length 39;
Best Local Similarity 75.8%; Pred. No. 4.4e+06;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 2108 TCTTTTATTAATATATATTTTCAAT 2140
DB 7 TATATTTTATTAATAAATTTATTAAT 39

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RESULT 97
LOCUS HSU26975/c 45 bp mRNA linear PRI 10-JUN-1995
DEFINITION Human isolate M15 T-cell receptor V-alpha 3/J alpha 57 junction
mRNA, partial cds.
ACCESSION U26975
VERSION U26975.1 GI:857421
KEYWORDS Homo sapiens.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 45)
AUTHORS Dave, V.P., Larche, M., Rencher, S.D., Koop, B.F. and Hurwitz, J.L.
TITLE Restricted usage of T-cell receptor V alpha sequence and
variable-jointing pairs after normal T-cell development and bone
marrow transplantation
JOURNAL Hum. Immunol. 37 (3), 178-184 (1993)
MEDLINE 94064390
PUBMED 8244780
REFERENCE 2 (bases 1 to 45)
AUTHORS Hurwitz, J.L.
TITLE Direct Submission
JOURNAL Submitted (12-MAY-1995) Julia L. Hurwitz, Immunology, St. Jude
Children's Research Hospital, 332 N. Lauderdale, Memphis, TN 38101,
USA
FEATURES
source location/Qualifiers
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/organism="Homo sapiens"
/isolate="M15"
/db_xref="taxon:9606"
/cblseq_type="blood"
CDS
1..>45
/note="encodes V alpha 3/J alpha 57 junction"
/codon_start=1
/evidence="experimental"
/product="T-cell receptor"
/protein_id="AAA68158.1"
/db_xref="GI:857422"
/translation="PCATDPWGSEKLVF"
BASE COUNT 7 a 10 c 14 g 14 t
ORIGIN
Query Match 0.9%; Score 20.2; DB 9; Length 45;
Best Local Similarity 68.3%; Pred. No. 4.5e+06;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
Qy 1547 AAAAACAAGCTTTTCCCATGATCTCCAAAGCCAGAGCAC 1587
Db 45 AAAAGCAGCTTTTGATCCGCCCAAGGGTCCGTAGCAC 5
RESULT 98
LOCUS AR032407 48 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 19 from patent US 5869241.
ACCESSION AR032407
VERSION AR032407.1 GI:5948012
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 48)
AUTHORS Edwards, C.A., Cantor, C.R., Andrews, B.M., Turin, L.M. and Fry, K.E.
TITLE Method of determining DNA sequence preference of a DNA-binding
molecule
JOURNAL Patent: US 5869241-A 19 09-FEB-1999;
FEATURES location/Qualifiers
source 1..48
/organism="unknown"
BASE COUNT 20 a 8 c 6 g 14 t
ORIGIN

Query Match 0.9%; Score 20.2; DB 6; Length 48;
Best Local Similarity 68.3%; Pred. No. 4.5e+06;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
Qy 2082 GATGTTTACGCAACCACTGAACTCTTTTATATA 2122
Db 1 GATGTTACACAGCAACAAATAATATCTGTGCAATATA 41
RESULT 99
LOCUS AR209071 48 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 19 from patent US 6384208.
ACCESSION AR209071
VERSION AR209071.1 GI:21510392
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 48)
AUTHORS Edwards, C.A., Cantor, C.R., Andrews, B.M., Turin, L.M. and Fry, K.E.
TITLE Sequence directed DNA binding molecules compositions and methods
JOURNAL Patent: US 6384208-A 19 07-MAY-2002;
FEATURES location/Qualifiers
source 1..48
/organism="unknown"
BASE COUNT 20 a 8 c 6 g 14 t
ORIGIN
Query Match 0.9%; Score 20.2; DB 6; Length 48;
Best Local Similarity 68.3%; Pred. No. 4.5e+06;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
Qy 2082 GATGTTTACGCAACCACTGAACTCTTTTATATA 2122
Db 1 GATGTTACACAGCAACAAATAATATCTGTGCAATATA 41
RESULT 100
LOCUS I29147 48 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 19 from patent US 5578444.
ACCESSION I29147
VERSION I29147.1 GI:1819938
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 48)
AUTHORS Edwards, C.A., Cantor, C.R., Andrews, B.M., Turin, L.M. and Fry, K.E.
TITLE Sequence-directed DNA-binding molecules compositions and methods
JOURNAL Patent: US 5578444-A 19 26-NOV-1996;
FEATURES location/Qualifiers
source 1..48
/organism="unknown"
BASE COUNT 20 a 8 c 6 g 14 t
ORIGIN
Query Match 0.9%; Score 20.2; DB 6; Length 48;
Best Local Similarity 68.3%; Pred. No. 4.5e+06;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
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Db 1 GATGTTACACAGCAACAAATAATATCTGTGCAATATA 41
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